

QY 241 GACAGCTTCAGCCGCCCTCACC GGTTCACTTCTCAGCCCTGCAGATCCTGCCCTACAC 300
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ACCESSION BC050416
VERSION BC050416.2 GI:34194585
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullehy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butcherfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

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12477932
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TITLE
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Strausberg,R.
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Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 25, 2003 this sequence version replaced gi:29791944.
Contact: MGC help desk
Email: cgabbs-rc@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES
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ORIGIN									
Query Match									
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AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepley,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: US 6512094-A 703 28-JAN-2003;		
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AR400442 2904 bp DNA linear PAT 18-DEC-2003
LOCUS AR400442
DEFINITION Sequence 703 from patent US 6620922.
ACCESSION AR400442
VERSION AR400442.1 GI:40143818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2904)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 703 16-SEP-2003;
FEATURES location/Qualifiers
Source 1..2904
/organism="unknown"
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ORIGIN
Query Match 97.0%; Score 2088; DB 6; Length 2904;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1773	AGGGAGGCCAGAAAGGGCTCCATGCACCTGGAATGCGGGGACTCTGCAGGTGATTACCAG	1832
QY	1085	GCTCAGGGTTAACAGCTTACCTCCTAGTTGAGACACACTAGAGAAAGGTTTTGGGAGC	1144
Db	1833	GCTCAGGGTTAACAGCTTACCTCCTAGTTGAGACACACTAGAGAAAGGTTTTGGGAGC	1892
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Db	2073	CCCACAGCAGCTGTCTTTTGTGCTGATCCACCCCCCTTACTTTTATCAGAGATGTGGCT	2132
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Db	2193	AACAAAGTAGAAGGAATCCATTGCTAGCTTTTCTGTGTGTGCTAATAATTTGGTAG	2252
QY	1505	GGTGGGGGATCCCCAACATCAGTCCCTGAGATAGCTGTCATTGGCGTATCATTC	1564
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QY	1565	CAGAACTTCTTCTCCTGGGGCTGGCCCCCAAATGCTTAACCCAGACCTTGGAAAT	1624
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QY	1625	TCTACTCATCCCAATGATAATCCAAATGCTGTACCAGGTTAGGGTGTTGAAGAA	1684
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QY	1985	GCACCCCTGCTGAGCTAAGGAGGTCTTATCTCTCAGGGGGGTTTAACTGCCGTTTG	2044
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RESULT 5				
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LOCUS	AR405709	2904 bp	DNA	linear
DEFINITION	Sequence 703 from patent US 6630305.			PAT 18-DEC-2003
ACCESSION	AR405709			
VERSION	AR405709.1	GI:40154546		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 2904)			
TITLE	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.			
	Compositions and methods for the therapy and diagnosis of prostate cancer			

JOURNAL Patent: US 6630305-A 703 07-OCT-2003;
FEATURES Location/Qualifiers
source 1..2904
/organism="unknown"
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ORIGIN

Query Match 97.0%; Score 2088; DB 6; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 GGCCTTCGGATGGGCAGCCTGGGGCTGTTCTCGACAGTGCGCCATCTCCCTGTTCTCT
Db 813 GGCCTTCGGATGGGCAGCCTGGGGCTGTTCTCGACAGTGCGCCATCTCCCTGTTCTCT
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Db 2133 GTTGTCTCTCTGTTGCCATCACAGACACAGGCATTTAAATATTAACTTATTATT 2192
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QY 1565 CAGAATCTTCTTCTCTGGGGTCTGGCCCCCAAAATGCTTAACCAAGACCTTGAAT 1624
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RESULT 6
AR564089
LOCUS AR564089 2904 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 703 from patent US 6759515.
ACCESSION AR564089
VERSION AR564089.1 GI:53979140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2904)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6759515-A 703 06-JUL-2004;
FEATURES Location/Qualifiers
SOURCE 1..2904
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Query Match 97.0%; Score 2088; DB 6; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 GCGCTTCGATGGGAGGCTGGGGCTGTTCTGACAGTGCCCATCTCCCTGTTCTTCT 124
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RESULT 7
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LOCUS AX200994
DEFINITION Sequence 624 from Patent WO0151633.
ACCESSION AX200994
VERSION AX200994.1 GI:15390821
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 624 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
Source 1. 2904 /organism="Homo sapiens"
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ORIGIN

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DB 2253 GTTGGGGATCCCCCAACATCAGTCCCTGAGATAGCTGTGCTATTGGCTGATTC 2312
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RESULT 8
AX267729 2904 bp DNA linear PAT 26-OCT-2001
LOCUS AX267729
DEFINITION Sequence 703 from Patent WO0173032.
ACCESSION AX267729
VERSION AX267729.1 GI:16516401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedrick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 703 04-OCT-2001;

FEATURES CORIXA CORPORATION (US)
Source Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN
Query Match 97.0%; Score 2088; DB 6; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 65 GGCGTTCCGATGGGCAAGCCTGGGGCTGTTCTCTGACAGTGGCCATCTCCCTGTCTCTCT 124
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RESULT 9
AX327336 3320 bp DNA linear PAT 07-JAN-2002
LOCUS Sequence 1 from Patent WO0181577.
DEFINITION AX327336
ACCESSION AX327336
VERSION AX327336.1 GI:18097882
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Lau, T., Lin, R.J., Parkes, D., Parry, G., Schneider, D.W.,
Steinbrecher, R., van Heuvel, P.T. and Wu, J.
TITLE Dna encoding the prost 03 polypeptide
JOURNAL Patent: WO 0181577-A 1 01-NOV-2001;
SCHERING AKTIENSELSCHAFT (DE)
FEATURES
source location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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Db	1955	CACATTGGGGTGAAGGGCGCTGCTCACTGGGTCCAGCTCCCGCTCCTGTTAGCCCCAT	2014
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LOCUS	AR112294
DEFINITION	Sequence 15 from patent US 6130043.
ACCESSION	AR112294
VERSION	AR112294.1 GI:14092194
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2143) Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H. Reagents and methods useful for detecting diseases of the prostate Patent: US 6130043-A 15 10-OCT-2000; Location/Qualifiers 1..2143 /organism="unknown" /mol_type="unassigned DNA"
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Best Local Similarity	99.9%; Pred. No. 0;
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RESULT 11
AR278711
LOCUS AR278711 4034 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 704 from patent US 6512094.
ACCESSION AR278711
VERSION AR278711.1 GI:29712957
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4034)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 704 28-JAN-2003;
FEATURES Location/Qualifiers
SOURCE 1..4034
/organism="unknown"
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Query Match 91.4%; Score 1968; DB 6; Length 4034;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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LOCUS AR400443 Sequence 704 from patent US 6620922.
DEFINITION AR400443
ACCESSION AR400443
VERSION AR400443.1 GI:40143820
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4034)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITILE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 704 16-SEP-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR405710 4034 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 704 from patent US 6630305.
ACCESSION AR405710
VERSION AR405710.1 GI:40154547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4034)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 704 07-OCT-2003;
FEATURES Location/Qualifiers
SOURCE 1. 4034
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Query Match 91.4%; Score 1968; DB 6; Length 4034;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DEFINITION	Sequence 704 from patent US 6759515.		
ACCESSION	ARS64090		
VERSION	ARS64090.1	GI:53979141	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 4034)		

AUTHORS			
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.			
TITLE			
Compositions and methods for the therapy and diagnosis of prostate cancer			
JOURNAL			
Patent: US 6759515-A 704 06-JUL-2004;			
FEATURES			
Source			
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Query Match			
Best Local Similarity 91.4%; Score 1968; DB 6; Length 4034;			
Matches 2088; Conservativity 100.0%; Pred.No. 0; Mismatches 0; Indels 1; Gaps 1;			
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QY	304	GGCTTCCCTTACCAACGGGAGAGAGAGTGTCTCTGCCAATAACGAGGGGACACTGG	363
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Db	3862	AGCACCCCTGCTGAGCTAAGGAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTT	3921
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Db	3922	GCAATTAATGCTGCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAACAATC	3981
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LOCUS			
DEFINITION Sequence 625 from Patent WO0151633.			
ACCESSION AX200995			
VERSION AX200995.1 GI:15390822			
KEYWORDS			
SOURCE			
ORGANISM Homo sapiens (human)			
REFERENCE			
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.			
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Query Match 91.4%; Score 1968; DB 6; Length 4034;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;			
QY	64	AGGCGTTGAGATGGGAGACCTGCGGCTGTCCTGACGTGCGCCATCTCCTGCTTCTC	123
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QY	124	TCTGTCATGACCGGCTGTGTGACGCGATTCGGCACTGAGCAGTCTATTGGCCAGTGT	183
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 2152

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Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Listing first 45 summaries

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8: gb_g881: *
9: gb_g882: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ALIGNMENTS

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 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL PUBMED 14671302
 REFERENCE 2 (bases 1 to 1626)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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DEFINITION AGENCOURT 10810630 MAPcL Homo sapiens cDNA clone IMAGE:6722106 5', mRNA sequence.

ACCESSION CA489628 GI:24952419

VERSION CA489628.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 897)

AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: csabbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM14284 row: e column: 18
High quality sequence stop: 625.

FEATURES

source

1..897

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6722106"

/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCaP"

/lab_host="EMDH10B"

/lab_host="EMDH10B"

/clone_lib="MAPcL"

/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

ORIGIN

Query Match 30.5%; Score 656; DB 6; Length 897;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 656; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCTGTACAGGGCGTGGCCAGAGCTGAGCCGGGACCGAGGCCGAGACACTATGA 60

Db 3 GGGGCTGTACAGGGCGTGGCCAGAGCTGAGCCGGGACCGAGGCCGAGACACTATGA 62

Qy 61 TGAAGGCGTTCGATGGGAGAGCTGGGCTGTCTCTGACAGTGGCCATCTCCCTGTCTT 120

Db 63 TGAAGGCGTTCGATGGGAGAGCTGGGCTGTCTCTGACAGTGGCCATCTCCCTGTCTT 122

Qy 121 CTCTGTGTCATGAGCCGGCTGTGTGACGATTGGCACTGAGCAGTCTATTGGCCAG 180

Db 123 CTCTGTGTCATGAGCCGGCTGTGTGACGATTGGCACTGAGCAGTCTATTGGCCAG 182

Qy 181 TGTGCACTTTCCTGTGGCTGCCGCTGCCACATGCTGTGTCACAGTGTGGCCGTGT 240

Db 183 TGTGCACTTTCCTGTGGCTGCCGCTGCCACATGCTGTGTCACAGTGTGGCCGTGT 242

Qy 241 GACAGTTACAGCCGCTCAGCCGGTTCACCTTCTAGCCCTGAGATCCTGCCCTACAC 300

Db 243 GACAGTTACAGCCGCTCAGCCGGTTCACCTTCTAGCCCTGAGATCCTGCCCTACAC 302

Qy 301 ACTGGCTCCCTTACACCGGGAGACAGGTGTTCTGCCCCAATAACGAGGGACAC 360

Db 303 ACTGGCTCCCTTACACCGGGAGACAGGTGTTCTGCCCCAATAACGAGGGACAC 362

Qy 361 TGGAGTGTACAGTAGAGACAGCTGATGACACAGCTTCTGTCAGGCCCTAAGCCTGG 420

Db 363 TGGAGTGTACAGTAGAGACAGCTGATGACACAGCTTCTGTCAGGCCCTAAGCCTGG 422

Qy 421 AGCTCCCTTCCCTAATGACACAGTGGGTGCTGAGGACAGTGGCTGCTCCACCTCCACC 480

Db 423 AGCTCCCTTCCCTAATGACACAGTGGGTGCTGAGGACAGTGGCTGCTCCACCTCCACC 482

Qy 481 CGGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGGTGAGCCAC 540

Db 483 CGGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGGTGAGCCAC 542

Qy 541 CGAGGCCAGGGTGTTCGGGGCCGGGCATCTGCTGACCTGACCTGACCTCTGATAGTC 600

Db 543 CGAGGCCAGGGTGTTCGGGGCCGGGCATCTGCTGACCTGACCTGACCTCTGATAGTC 602

Qy 601 CTCTCTGTGTCCAGAGTGGGCCCATCCCTGTTATGGGCTTCATTGCCAGCTCA 656

Db 603 CTCTCTGTGTCCAGAGTGGGCCCATCCCTGTTATGGGCTTCATTGCCAGCTCA 658

RESULT 6

BU689021/c

LOCUS 670 bp mRNA linear EST 07-OCT-2002

DEFINITION UI-CF-EC1-ady-f-04-0-UI-61 UI-CF-EC1 Homo sapiens cDNA clone

UI-CF-EC1-ady-f-04-0-UI 3', mRNA sequence.

ACCESSION BU689021

VERSION BU689021.1

KEYWORDS GI:23546376

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

REFERENCE 1 (bases 1 to 670)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalizaton and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).

The following repetitive elements were found in this cDNA sequence: 1-28, >AT rich#low_complexity

Seq primer: M13 FORWARD

POLYA=yes.

FEATURES

source

1..670

Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-ECl-ady-f-04-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-ECl"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-ECl is a normalized cDNA library containing the following tissue(s): Normal Lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_LIB=UI-CF-ECl
TAG_SEQ=AAGTGGCTTAC"

ORIGIN

Query Match 29.9%; Score 644; DB 5; Length 670;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1509 GGGGATCCCAACAATCAGGTCCCTGAGATAGCTGTGCTATGGGCTGATCATTTGCCAGA 1568
DB 661 GGGGATCCCAACAATCAGGTCCCTGAGATAGCTGTGCTATGGGCTGATCATTTGCCAGA 602
QY 1569 ATCTTCTTCTCTGGGGTCTGGCCCCCAAAATGCTTAACCCAGACGACCTTGAATTTCTA 1628
DB 601 ATCTTCTTCTCTGGGGTCTGGCCCCCAAAATGCTTAACCCAGACGACCTTGAATTTCTA 542
QY 1629 CTCATCCCAAAATGATTAATTCCAAATGCTGTTACCCAAAGTTAGGGTGTGAAGAAAGTTA 1688
DB 541 CTCATCCCAAAATGATTAATTCCAAATGCTGTTACCCAAAGTTAGGGTGTGAAGAAAGTTA 482
QY 1689 GAGGGTGGGCTTCAGGTCTCAACGGCTTCCCTAACCAACCCCTTCTCTTGCCCCAGCC 1748
DB 481 GAGGGTGGGCTTCAGGTCTCAACGGCTTCCCTAACCAACCCCTTCTCTTGCCCCAGCC 422
QY 1749 TGGTTCCTCCCACTTCCACTCCCTCTACTCTCTTAAGACTGGGCTGATGAAGGCACTG 1808
DB 421 TGGTTCCTCCCACTTCCACTCCCTCTACTCTCTTAAGACTGGGCTGATGAAGGCACTG 362
QY 1809 CCCAAATTTCCCTACCCCACTTTCCCTACCCCACTTTCCCAAGCTTCCACA 1868
DB 361 CCCAAATTTCCCTACCCCACTTTCCCTACCCCACTTTCCCAAGCTTCCACA 302
QY 1869 ACCCTGTTGAGCTACTGCAGACCAAGACCAAAAGTGGGTTTCCCAAGCTTGTGTC 1928
DB 301 ACCCTGTTGAGCTACTGCAGACCAAGACCAAAAGTGGGTTTCCCAAGCTTGTGTC 242
QY 1929 CATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAATCTCACAGAAACTCAGAGCAC 1988
DB 241 CATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAATCTCACAGAAACTCAGAGCAC 182
QY 1989 CCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAGTCCGTTGCAAT 2048
DB 181 CCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAGTCCGTTGCAAT 122
QY 2049 AATGTCGCTTATTATTAGCGGGGTGAATATTTTACTGTAGTGAATCAGAGT 2108
DB 121 AATGTCGCTTATTATTAGCGGGGTGAATATTTTACTGTAGTGAATCAGAGT 62

QY 2109 ATAAATGTTATGGTGACAAATTAAGGCTTCTTATATGTTTA 2152
DB 61 ATAAATGTTATGGTGACAAATTAAGGCTTCTTATATGTTTA 18

RESULT 7
CB048223
LOCUS
DEFINITION
NISC_g103cell.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3270644
5', mRNA sequence.
ACCESSION
CB048223
VERSION
CB048223.1 GI:27786510
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM8006 row: J column: 21
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..651

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3270644"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP_Pr22 was prepared, and 88
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 29.6%; Score 638; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1462 TCCATGCTAGCTTTCTGTGTGGTGTCTAATATTTGGGTAGGGTGGGATCCCAAC 1521
DB 14 TCCATGCTAGCTTTCTGTGTGGTGTCTAATATTTGGGTAGGGTGGGATCCCAAC 73
QY 1522 AATCAGGTCCTCCCTGAGATAGCTGTCATTGGGCTGATCATTTGCCAGAATCTTCTTCT 1581
DB 74 AATCAGGTCCTCCCTGAGATAGCTGTCATTGGGCTGATCATTTGCCAGAATCTTCTTCT 133
QY 1582 GGGGTGCGCCCCCAAAATGCTTAACCCAGACCTTGAATTTCTACTCATCCCAATG 1641
DB 134 GGGGTGCGCCCCCAAAATGCTTAACCCAGACCTTGAATTTCTACTCATCCCAATG 193
QY 1642 ATAAATCCAATGCTGTTACCCAAGTTAGGGTGTGAAGGAAGGTAGAGGGTGGGCTT 1701
DB 194 ATAAATCCAATGCTGTTACCCAAGTTAGGGTGTGAAGGAAGGTAGAGGGTGGGCTT 253

QY 1702 CAGGTCCTCAACGGCTTCCCTAACACCCCTCTTCTCTGGCCCAAGCTGTCCCCAC 1761
|||||
Db 254 CAGGTCCTCAACGGCTTCCCTAACACCCCTCTTCTCTGGCCCAAGCTGTCCCCAC 313
QY 1762 TTCCACTCCCTCTACTCTCTAGAGCTGGGCTGATGAAGGCACTGCCAAATTTC 1821
|||||
Db 314 TTCCACTCCCTCTACTCTCTAGAGCTGGGCTGATGAAGGCACTGCCAAATTTC 373
QY 1822 CTACCCCCAACTTTCCCTACCCCACTTTCCCAAGCTTCACAACCCTGTTGGAG 1881
|||||
Db 374 CTACCCCCAACTTTCCCTACCCCACTTTCCCAAGCTTCACAACCCTGTTGGAG 433
QY 1882 CTACTGACGAGACCAAGACCAAAAGTCCGCTTCCCAAGCTTTGTCATCTCAGCCCC 1941
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Db 434 CTACTGACGAGACCAAGACCAAAAGTCCGCTTCCCAAGCTTTGTCATCTCAGCCCC 493
QY 1942 AGAGTATATCTGTGCTTGGGGAATCTCACACAGAACTCAGAGACACCCCTGCTGAGC 2001
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Db 494 AGAGTATATCTGTGCTTGGGGAATCTCACACAGAACTCAGAGACACCCCTGCTGAGC 553
QY 2002 TAAGGAGGCTTATCTCTCAGGGGGGTTAAGTGCCGTTGCAATAATGTCCTTAT 2061
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Db 554 TAAGGAGGCTTATCTCTCAGGGGGGTTAAGTGCCGTTGCAATAATGTCCTTAT 613
QY 2062 TTATTAGCGGGGTGAATATTTTAATCTGTAAGTGAGC 2099
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Db 614 TTATTAGCGGGGTGAATATTTTAATCTGTAAGTGAGC 651

RESULT 8
BQ950912 916 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT 8754471 lupsk1_sciatic_nerve Homo sapiens cDNA clone
DEFINITION IMAGE:6205362 5', mRNA sequence.
ACCESSION BQ950912
VERSION BQ950912.1 GI:22366390
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 916)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13628 row: b column: 19
High quality sequence stop: 579.
Location/Qualifiers

FEATURES
source 1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGCTCG-3' and
5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN
Query Match 28.7%; Score 617; DB 5; Length 916;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1101 TAGCCTCCTAGTTGAGACACCTAGAGAAGGTTTGGAGCTGAATAAAGTCA 1160
|||||
Db 1 TAGCCTCCTAGTTGAGACACACCTAGAGAAGGTTTGGAGCTGAATAAAGTCA 60
QY 1161 CTTGGTTTCCCATCTCTAAGCCCCCTTAACCTGCAGCTTCGTTAATAGTCTGCA 1220
|||||
Db 61 CTTGGTTTCCCATCTCTAAGCCCCCTTAACCTGCAGCTTCGTTAATAGTCTGCA 120
QY 1221 GGAGTTTCTAGATGAACACTCTCCATGGGATTGAACATATGAAGTTATTG 1280
|||||
Db 121 GGAGTTTCTAGATGAACACTCTCCATGGGATTGAACATATGAAGTTATTG 180
QY 1281 GGAAGAGTCTGAGGGGCAACACAGAAGACAGGTCCTCAGCCACAGCACTGCTT 1340
|||||
Db 181 GGAAGAGTCTGAGGGGCAACACAGAAGACAGGTCCTCAGCCACAGCACTGCTT 240
QY 1341 TTTCGTGATCCACCCCTCTTACCTTTATCAGAGTGGCCTGTGCTCTGTTG 1400
|||||
Db 241 TTTCGTGATCCACCCCTCTTACCTTTATCAGAGTGGCCTGTGCTCTGTTG 300
QY 1401 CCATCACAGAGACAGGCAATTAATTTAATCTTATTATTAACAAGTAGAAGGA 1460
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Db 301 CCATCACAGAGACAGGCAATTAATTTAATCTTATTATTAACAAGTAGAAGGA 360
QY 1461 ATCATTGCTAGCTTTTCTGTGTTGCTCTAATATTGGGTAGGGATCCCAA 1520
|||||
Db 361 ATCATTGCTAGCTTTTCTGTGTTGCTCTAATATTGGGTAGGGATCCCAA 420
QY 1521 CAATCAGGTCCTCCTAGATAGCTGTCATTGGGCTGATCATGCGAATCTTCTCC 1580
|||||
Db 421 CAATCAGGTCCTCCTAGATAGCTGTCATTGGGCTGATCATGCGAATCTTCTCC 480
QY 1581 TGGGCTCTGGCCCCCAAAATGCTTAACCCAGAGACCTTGAAATCTACTCATCCAA 1640
|||||
Db 481 TGGGCTCTGGCCCCCAAAATGCTTAACCCAGAGACCTTGAAATCTACTCATCCAA 540
QY 1641 GATTAATCCCAATGCTGTTAACCAGGTTAGGCTGTTGAAGGAAGTAGAGGTGGGCT 1700
|||||
Db 541 GATTAATCCCAATGCTGTTAACCAGGTTAGGCTGTTGAAGGAAGTAGAGGTGGGCT 600
QY 1701 TCAGGTCCTCAACGGCTT 1717
|||||
Db 601 TCAGGTCCTCAACGGCTT 617

RESULT 9
BQ950805 959 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT 8842232 lupsk1_sciatic_nerve Homo sapiens cDNA clone
DEFINITION IMAGE:6204253 5', mRNA sequence.
ACCESSION BQ950805
VERSION BQ950805.1 GI:22366283
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 959)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13625 row: d column: 14
High quality sequence start: 2
High quality sequence stop: 490.

FEATURES

Source

1. 959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204253"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic_nerve"
/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dt priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

Query Match 26.2%; Score 564; DB 5; Length 959;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 CGTGGTGTGAGGAGGAGTGGCTGTCTCCACCTCCACCCGCGCTTGCGGGGCTTGC 501
DB 7 CGTGGTGTGAGGAGGAGTGGCTGTCTCCACCTCCACCCGCGCTTGCGGGGCTTGC 66
QY 502 CTGTGATGTCTCCGTACGTGTGTGTGGGTGAGCCACCGAGGCCAGGGTGTTCGGG 561
DB 67 CTGTGATGTCTCCGTACGTGTGTGTGGGTGAGCCACCGAGGCCAGGGTGTTCGGG 126
QY 562 CCGGGGCACTGCTCTGGAACCTCGCCATCTGATAGTGCCTTCTCTGCTGCCAGGTGC 621
DB 127 CCGGGGCACTGCTCTGGAACCTCGCCATCTGATAGTGCCTTCTCTGCTGCCAGGTGC 186
QY 622 CCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGT 681
DB 187 CCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGT 246
QY 682 GTCTGCCGAGGCTGGGTCTGTGTGCCATTACTTTGTCTACACAGGTAGTATTGACAA 741
DB 247 GTCTGCCGAGGCTGGGTCTGTGTGCCATTACTTTGTCTACACAGGTAGTATTGACAA 306
QY 742 GAGCGACTGGCCAAATACTCAGCGTAGAAAACTTCCAGACATTGGGGTGAGGGCCTG 801
DB 307 GAGCGACTGGCCAAATACTCAGCGTAGAAAACTTCCAGACATTGGGGTGAGGGCCTG 366
QY 802 CCTCACTGGGTCCAGCTCCCGCTCTGTAGCCCAATGGGGGTGCGGGGCTGCCGCC 861
DB 367 CCTCACTGGGTCCAGCTCCCGCTCTGTAGCCCAATGGGGGTGCGGGGCTGCCGCC 426
QY 862 AGTTTCTGTGTGCAAGTAATGTGGCTCTGTGTGCCACCTGTGTGTGAAGTGC 921
DB 427 AGTTTCTGTGTGCAAGTAATGTGGCTCTGTGTGCCACCTGTGTGTGAAGTGC 486
QY 922 GTAGCTGCACAGCTGGGGGTGGGGGTGCCCTCTCTCTCTCCCAAGTCTTAAGGGTGC 981
DB 487 GTAGCTGCACAGCTGGGGGTGGGGGTGCCCTCTCTCTCTCCCAAGTCTTAAGGGTGC 546

QY 982 CTGACTGAGAGCCCTTCCAAGGGG 1005
DB 547 CTGACTGAGAGCCCTTCCAAGGGG 570

RESULT 10 718 bp mRNA linear EST 20-OCT-2000
BE867241
LOCUS BE867241
DEFINITION 601442309F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846411 5',
mRNA sequence.
ACCESSION BE867241
VERSION BE867241.1 GI:10316017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL 1 (bases 1 to 718)
COMMENT NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9559 row: a column: 04
High quality sequence stop: 693.

FEATURES

Source

1. 718
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3846411"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_65"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 25.1%; Score 541; DB 2; Length 718;
Best Local Similarity 100.0%; Pred. No. 3.6e-279;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 TCTGTATGAGACCGGCTGTGTGACGATTGGGCACTGACAGTCTATTGGCCAGTGT 183
DB 1 TCTGTATGAGACCGGCTGTGTGACGATTGGGCACTGACAGTCTATTGGCCAGTGT 60
QY 184 GGCAGCTTTCCCTGTGGCTGCGCGTGCCACATGCTGTGCCACAGTGTGCGGTGAC 243
DB 61 GGCAGCTTTCCCTGTGGCTGCGCGTGCCACATGCTGTGCCACAGTGTGCGGTGAC 120
QY 244 AGCTTACGCGCCCTCACCGGTTCACTTCTCAGCCCTGCAGATCTGCCCTACACT 303
DB 121 AGCTTACGCGCCCTCACCGGTTCACTTCTCAGCCCTGCAGATCTGCCCTACACT 180
QY 304 GGCCTCCCTCTACACCGGGAAGCAGGTGTTCTGCCCCAATAACGAGGGGACACTGG 363
DB 181 GGCCTCCCTCTACACCGGGAAGCAGGTGTTCTGCCCCAATAACGAGGGGACACTGG 240
QY 364 AGGTGTAGCAGTAGAGCAGCCTGATGACCAAGCTTCTGCGAGGCCCTTAAGCCTGAGC 423
DB 241 AGGTGTAGCAGTAGAGCAGCCTGATGACCAAGCTTCTGCGAGGCCCTTAAGCCTGAGC 300
QY 424 TCCCTTCCCTATGACACGTGGGTGTGTGAGGAGTGGCTGTCCCACTTCAACCCGC 483

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Db      301 TCCCTTCCTTAATGACACAGTGGGTGAGGAGCAGTGGCTGTCCACCTCCACCCGC 360
Qy      484 GCTTCGGGGGCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGA 543
Db      361 GCTTCGGGGGCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGA 420
Qy      544 GGCCAGGGTGTTCGGGGCGGGCACTGTGACCTGGACCTGCCATCCTGGATAGTGCCT 603
Db      421 GGCCAGGGTGTTCGGGGCGGGCACTGTGACCTGGACCTGCCATCCTGGATAGTGCCT 480
Qy      604 CCTGCTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTCCAGTCAAGCAGTC 663
Db      481 CCTGCTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTCCAGTCAAGCAGTC 540
Qy      664 T 664
Db      541 T 541
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RESULT 11

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LOCUS      CN373214      581 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION 1700532189001 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN373214
VERSION    CN373214.1 GI:47373148
KEYWORDS   EST.
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SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 581)

TITLE
JOURNAL Li, Y., Xu, C., Fang, R., Guebler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com

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FEATURES
source
1. 581
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tisue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_lib="GRN_ES"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 24.5%; Score 528; DB 7; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.6e-272;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1161 CCTGGTTCCCATCTCTAAGCCCTTAACCTGCAGCTTCGTTAATGATGCTCTGCATG 1220
Db      39 CCTGGTTCCCATCTCTAAGCCCTTAACCTGCAGCTTCGTTAATGATGCTCTGCATG 98
Qy      1221 GGAGTTTCTAGATGAACACTCTCTCATGGGATTGAAACATATGAAAGTTATTGTAGG 1280
Db      99 GGAGTTTCTAGATGAACACTCTCTCATGGGATTGAAACATATGAAAGTTATTGTAGG 158
Qy      1281 GGAAGGTCCTGAGGGGCAACACAGAACCAGGTCCCTCAGCCCAACAGCACTGTCTT 1340
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Db      159 GGAAGGTCCTGAGGGGCAACACAGAACCAGGTCCCTCAGCCCAACAGCACTGTCTT 218
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Db      219 TTGCTGATCCACCCCTCTTACCTTTATCAGGATGTGGCTGTGCTCTGTG 278
Qy      1401 CCATCAGAGACACAGGCATTAAATTTAACTTATTATTAAACAAAGTAGAAGGA 1460
Db      279 CCATCAGAGACACAGGCATTAAATTTAACTTATTATTAAACAAAGTAGAAGGA 338
Qy      1461 ATCAATTGCTAGCTTTTCTGTGTGTGTCTAATATTGGGTAGGGTGGGATCCCAA 1520
Db      339 ATCAATTGCTAGCTTTTCTGTGTGTGTCTAATATTGGGTAGGGTGGGATCCCAA 398
Qy      1521 CAATCAGTCCCTGAGATAGCTGTGATTGGGCTGATCATGCCAGATCTTCTTCC 1580
Db      399 CAATCAGTCCCTGAGATAGCTGTGATTGGGCTGATCATGCCAGATCTTCTTCC 458
Qy      1581 TGGGTCCTGGCCCCCAAAATGCTTAACCCAGACCTTGAATTTCTACTATCCCAAT 1640
Db      459 TGGGTCCTGGCCCCCAAAATGCTTAACCCAGACCTTGAATTTCTACTATCCCAAT 518
Qy      1641 GATAATTCCAATGTGTGTACCCAGGTTAGGGTGTGAAGGAAGTA 1688
Db      519 GATAATTCCAATGTGTGTACCCAGGTTAGGGTGTGAAGGAAGTA 566
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RESULT 12

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LOCUS      BG469586      589 bp      mRNA      linear      EST 21-MAR-2001
DEFINITION 602533622F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661500 5',  
mRNA sequence.
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ACCESSION BG469586
VERSION BG469586.1 GI:13401861
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 589)

TITLE
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML460 row: k column: 05
High quality sequence stop: 587.

FEATURES
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1. 589
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
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/tisue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 15"
/note="Organ: colon; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 22.1%; Score 491; DB 4; Length 589;
Best Local Similarity 100.0%; Pred. No. 3.1e-252;
Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CTGCAGCTTCGTTAATGAGCTCTTGATGGAGTTTCTAGATGAACACTCTCCAT 1249
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Db 2 CTGCAGCTTCGTTAATGAGCTCTTGATGGAGTTTCTAGATGAACACTCTCCAT 61
1250 GGGATTTGAACATATGAAGTTATTTGTAGGGGAGAGTCTGAGGGGCAACACAGA 1309
|||||
Db 62 GGGATTTGAACATATGAAGTTATTTGTAGGGGAGAGTCTGAGGGGCAACACAGA 121
1310 ACCAGTCCCTCAGCCACAGCACTGTCTTTTGTGATCCACCCCTCTTACCTTTT 1369
|||||
Db 122 ACCAGTCCCTCAGCCACAGCACTGTCTTTTGTGATCCACCCCTCTTACCTTTT 181
1370 ATCAGATGTGGCTGTGCTCTTCTGTTGCCATCAGAGACACAGGCAATTAAATAT 1429
|||||
Db 182 ATCAGATGTGGCTGTGCTCTTCTGTTGCCATCAGAGACACAGGCAATTAAATAT 241
1430 TTAATCTATTATTAAACAAGTAGAAGGGAATCCATTGCTAGCTTTCTGTGTTGTT 1489
|||||
Db 242 TTAATCTATTATTAAACAAGTAGAAGGGAATCCATTGCTAGCTTTCTGTGTTGTT 301
1490 CTAATATTTGGGTAGGGTGGGGGATCCCAACAATCAGGTCCCTGAGATAGCTGTCAT 1549
|||||
Db 302 CTAATATTTGGGTAGGGTGGGGGATCCCAACAATCAGGTCCCTGAGATAGCTGTCAT 361
1550 TGGGCTGATCATGTCAGAAATCTTCTCTCTGGGGTCTGGCCCCCAAAATGCTTAAC 1609
|||||
Db 362 TGGGCTGATCATGTCAGAAATCTTCTCTCTGGGGTCTGGCCCCCAAAATGCTTAAC 421
1610 CAGGACCTTGAAATCTACTCATCCCAATGATAATTCGAATGCTGTTACCAAGTT 1669
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Db 422 CAGGACCTTGAAATCTACTCATCCCAATGATAATTCGAATGCTGTTACCAAGTT 481
1670 AGGGTGTGAA 1680
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Db 482 AGGGTGTGAA 492

RESULT 13
BQ942028 875 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT 8817111 Lupski_sciatic_nerve Homo sapiens cDNA clone
DEFINITION IMAGE:6202754 5', mRNA sequence.
ACCESSION BQ942028
VERSION BQ942028.1 GI:22357506
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 875)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13621 row: f column: 03
High quality sequence stop: 417.
Location/Qualifiers
1..875
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/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:6202754"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

Query Match 22.1%; Score 475; DB 5; Length 875;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1285 GAGTCTGAGGGGCAACACAGAAGACAGGTCCCTCAGCCACAGCACTGCTTTTG 1344
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Db 1 GAGTCTGAGGGGCAACACAGAAGACAGGTCCCTCAGCCACAGCACTGCTTTTG 60
1345 CTGATCCACCCCTCTTAACCTTTATCAGAGATGCGCTGTGCTCTGTGCCAT 1404
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Db 61 CTGATCCACCCCTCTTAACCTTTATCAGAGATGCGCTGTGCTCTGTGCCAT 120
1405 CACAGAGACACAGGCAATTAAATATTAACTTAATTAAACAAGTAGAAGGAATCC 1464
|||||
Db 121 CACAGAGACACAGGCAATTAAATATTAACTTAATTAAACAAGTAGAAGGAATCC 180
1465 ATTGCTAGCTTTCTGTGTGGTGTCTAAATTTGGGTAGGGTGGGGATCCCAACAAT 1524
|||||
Db 181 ATTGCTAGCTTTCTGTGTGGTGTCTAAATTTGGGTAGGGTGGGGATCCCAACAAT 240
1525 CAGTCCCTGAGATAGCTGTGATGGGCTGATCATTTGCCAGAACTTCTTCTCTGGG 1584
|||||
Db 241 CAGTCCCTGAGATAGCTGTGATGGGCTGATCATTTGCCAGAACTTCTTCTCTGGG 300
1585 GTCTGCCCCCAAAATGCTTAACCCAGACCTTGGAATTTCTACTCATCCCAATGATA 1644
|||||
Db 301 GTCTGCCCCCAAAATGCTTAACCCAGACCTTGGAATTTCTACTCATCCCAATGATA 360
1645 ATTCCAATGCTGTTAACCAGGTTAGGGTGTGAAGGAAGTAGAGGTGGGCTTCAG 1704
|||||
Db 361 ATTCCAATGCTGTTAACCAGGTTAGGGTGTGAAGGAAGTAGAGGTGGGCTTCAG 420
1705 GTCTCAACGGCTTCCCTTAACCAACCCTCTTCTTGGCCAGCCTGTCCCC 1759
|||||
Db 421 GTCTCAACGGCTTCCCTTAACCAACCCTCTTCTTGGCCAGCCTGTCCCC 475

RESULT 14
BM914562 1060 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6615475 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480245
DEFINITION 5', mRNA sequence.
ACCESSION BM914562
VERSION BM914562.1 GI:19364941
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 1060)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: LNCM2002 row: m column: 14
High quality sequence stop: 485.
Location/Qualifiers

FEATURES

source

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/clone="IMAGE:5480245"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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ORIGIN

Query Match 22.0%; Score 474; DB 5; Length 1060;
Best Local Similarity 100.0%; Pred. No. 4.7e-243;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCTGCCAGGCCCTAAGCCTG 60
QY 420 GAGCTCCCTTCCCTAATGAGACACGTGGGTGCTGGAGGAGAGTGGCCTGCTCCACCTCCAC 479
Db 61 GAGCTCCCTTCCCTAATGAGACACGTGGGTGCTGGAGGAGAGTGGCCTGCTCCACCTCCAC 120
QY 480 CCGCGCTGCGGGGCTCTGCTGATGTCCTCGTACGTGTGTGGTGGTGAGGCCA 539
Db 121 CCGCGCTGCGGGGCTCTGCTGATGTCCTCGTACGTGTGTGGTGGTGAGGCCA 180
QY 540 CCGAGGCCAGGGTGTCCGGGCGGGGCATCTGCCTGAGCCTGCCATCTGGATAGTG 599
Db 181 CCGAGGCCAGGGTGTCCGGGCGGGGCATCTGCCTGAGCCTGCCATCTGGATAGTG 240
QY 600 CCTTCCTGCTGCCAGGTGGGCCCATCCCTGTTATGGGGCTCCATTGTCAGCTCAGCC 659
Db 241 CCTTCCTGCTGCCAGGTGGGCCCATCCCTGTTATGGGGCTCCATTGTCAGCTCAGCC 300
QY 660 AGTCTGTACTGCTTATATGTTGTCTGCGCCAGAGCCCTGGGTCTGGTCCATTACTTTG 719
Db 301 AGTCTGTACTGCTTATATGTTGTCTGCGCCAGAGCCCTGGGTCTGGTCCATTACTTTG 360
QY 720 CTACACAGGTAGTATTGTGACAAAGAGGACTTGGCCAAATACTCAGCGTAGAAAACTTCCA 779
Db 361 CTACACAGGTAGTATTGTGACAAAGAGGACTTGGCCAAATACTCAGCGTAGAAAACTTCCA 420
QY 780 GCACATGGGGGTGAGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 833
Db 421 GCACATGGGGGTGAGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474
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RESULT 15
LOCUS BX098291 515 bp mRNA linear EST 04-FEB-2003
DEFINITION BX098291 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE998P04693 ; IMAGE:308595, mRNA sequence.
ACCESSION BX098291
VERSION BX098291.1 GI:27843586
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 515)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.

Human Unigeneset - RZPD3

Unpublished (2003)

JOURNAL

COMMENT

Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998P04693.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972> Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCAACACAGAAACAGCTATGAC.

FEATURES

source

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1. 515
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998P04693 ; IMAGE:308595"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal lung NbHL19W"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGGAGGTGGGCTTCAAGTCTCAACGGCTTCCCTAAC
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."
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ORIGIN

Query Match 21.8%; Score 470; DB 5; Length 515;
Best Local Similarity 100.0%; Pred. No. 6.4e-241;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 94 AGTTAGGGTGTGAAGGAAGGTAGGGGTGGGCTTCAGGTCTCAACGGCTTCCCTAAC 153
QY 1725 CACCCTCTTCTTCTTGCCAGCCTGTTCCCCCACTTCCACTCCCTCTACTCTCTCT 1784
Db 154 CACCCTCTTCTTCTTGCCAGCCTGTTCCCCCACTTCCACTCCCTCTACTCTCTCT 213
QY 1785 AGGACTGGGCTGATGAAGGCATGCCAAATTTCCCTACCCCACTTCCCTACCC 1844
Db 214 AGGACTGGGCTGATGAAGGCATGCCAAATTTCCCTACCCCACTTCCCTACCC 273
QY 1845 CCAACTTTCCCAACAGCTCCACAACCTGTTTGGAGCTACTGACAGACAGACACAA 1904
Db 274 CCAACTTTCCCAACAGCTCCACAACCTGTTTGGAGCTACTGACAGACAGACACAA 333
QY 1905 AGTGGGTTTCCCAAGCCTTGTTCATCTCAGCCCCCAGAGTATATCTGTGCTGGGAA 1964
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Db 334 AGTGGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCAGAGTATATCTGTGCTTGGGGA 393
OY 1965 TCTCACACAGAACTCAGAGACCCCCCTGCTGAGCTTAAGGAGGTCTTATCTCAGG 2024
Db 394 TCTCACACAGAACTCAGAGACCCCCCTGCTGAGCTTAAGGAGGTCTTATCTCAGG 453
OY 2025 GGGGGTTTAAGTCCGTTTGCAATATGTGCTTATTTTAGCGGG 2074
Db 454 GGGGGTTTAAGTCCGTTTGCAATATGTGCTTATTTTAGCGGG 503

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-841-894A-15
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Sequence: 1 ACCAGGCGCTGCCAGAGCT.....AAGCTTTCTATATGTTTA 2143

Scoring table: OLIGO=NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	1970	91.9	3306	9	BC050416	BC050416 Homo sapi
4	1916	89.4	2904	6	AR278710	AR278710 Sequence
5	1916	89.4	2904	6	AR400442	AR400442 Sequence
6	1916	89.4	2904	6	AR405709	AR405709 Sequence
7	1916	89.4	2904	6	AR564089	AR564089 Sequence
8	1916	89.4	2904	6	AX200994	AX200994 Sequence
9	1916	89.4	2904	6	AX267729	AX267729 Sequence
10	1900	88.7	3320	6	AX327336	AX327336 Sequence
11	1796	83.8	4034	6	AR278711	AR278711 Sequence
12	1796	83.8	4034	6	AR400443	AR400443 Sequence
13	1796	83.8	4034	6	AR405710	AR405710 Sequence
14	1796	83.8	4034	6	AR564090	AR564090 Sequence
15	1796	83.8	4034	6	AX200995	AX200995 Sequence
16	1796	83.8	4034	6	AX267730	AX267730 Sequence
17	1764	82.3	4894	6	AR278709	AR278709 Sequence
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22	1764	82.3	4894	6	AX267728	AX267728 Sequence
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25	1739	81.1	3410	6	AR278229	AR278229 Sequence
26	1739	81.1	3410	6	AR366925	AR366925 Sequence
27	1739	81.1	3410	6	AR370821	AR370821 Sequence
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34	1739	81.1	3410	6	AX140620	AX140620 Sequence
35	1739	81.1	3410	6	AX200480	AX200480 Sequence
36	1739	81.1	3410	6	AX267136	AX267136 Sequence
37	1739	81.1	3410	6	AX429961	AX429961 Sequence
38	1739	81.1	3410	6	BD070258	BD070258 Compounds
39	1739	81.1	3410	9	AY033593	AY033593 Homo sapi
40	1651	77.0	6976	6	AR278712	AR278712 Sequence
41	1651	77.0	6976	6	AR400444	AR400444 Sequence
42	1651	77.0	6976	6	AR405711	AR405711 Sequence
43	1651	77.0	6976	6	AR564091	AR564091 Sequence
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ALIGNMENTS

RESULT 1
AR112294
LOCUS AR112294 2143 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 15 from patent US 6130043.
ACCESSION AR112294
VERSION AR112294.1 GI:14092194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2143)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.
TITLES Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 15 10-OCT-2000;
FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 2143; DB 6; Length 2143;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCAGGCGCTGCCAGAGCTGAGCGGCGACCGAGGCCCGAGACACTATGATGAAGCG 60
1 ACCAGGCGCTGCCAGAGCTGAGCGGCGACCGAGGCCCGAGACACTATGATGAAGCG 60
Db 1 ACCAGGCGCTGCCAGAGCTGAGCGGCGACCGAGGCCCGAGACACTATGATGAAGCG 60
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LOCUS	AR112295	2152 bp	DNA	linear
DEFINITION	Sequence 16 from patent US 6130043.			PAT 16-MAY-2001
ACCESSION	AR112295			
VERSION	AR112295.1	GI:14092195		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 2152)			
	Billings-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.			
TITLE	Reagents and methods useful for detecting diseases of the prostate			
JOURNAL	Patent: US 6130043-A 16 10-OCT-2000;			
FEATURES	Location/Qualifiers			

source 1..2152
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Query Match 92.0%; Score 1972; DB 6; Length 2152;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2142; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 301 CCCTCTACCAACGGGAGAGCAGGTGTTCTCTGCCCCAAATACCGAGGGAGACACTGAGGTG 360
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Db CTAGCAGTGAAGACAGCCTGATGATGACAGCTTCTGCGCAGGCCCTTAAGCCTGAGCTCCCT 428
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LOCUS BC050416 3306 bp mRNA linear PRI 30-JUN-2004

DEFINITION Homo sapiens prostein protein, mRNA (CDNA clone MGC:54090

IMAGE:6198823), complete cds.

ACCESSION BC050416

VERSION BC050416.2 GI:34194585

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3306)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mulahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 3306)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT On Aug 25, 2003 this sequence version replaced gi:29791944.

Contact: MGC help desk

Email: cgabs-rc@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES

source location/Qualifiers

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Matches 2140; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 3249 AATACTTTATGTTGACAAATTAAGGCTTCTTATATGTT 3290

RESULT 4
AR278710
LOCUS AR278710 2904 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 703 from patent US 6512094.
ACCESSION AR278710
VERSION AR278710.1 GI:29712956
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2904)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 703 28-JAN-2003;
FEATURES Location/Qualifiers
source 1..2904
/organism="unknown"
/mol_type="genomic DNA"

Query Match 89.4%; Score 1916; DB 6; Length 2904;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 417 CCCTTCCCTAATGAGACACGTGGGTGTGAGAGCAGTGGCCTGTCCACCTCCACCCGCG 476

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Db 1413 GTCACTGCTATATGTGTGTCTGCCGACGGCTGGGTCTGTCGCCATTTACTTTGCTACA 1472

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Db 1473 CAGTAGTATTGACAAGAGCGACTTGGCCAATACTCAGCGTAGAAAACTTCCAGCACA 1532

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Db 1533 TTGGGGTGAAGGGCTGCTCTCAGTGGGTCCAGCTCCCCGCTCTGTAGCCCCATGGGG 1592

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Db 2253 GGTGGGGGATCCCCCAAAATCAGGTCCCCCTGAGATAGCTGTCAATTGGGCTGATTC 2312

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Db 2313 CAGAACTTCTTCTCTGCGGGTCTGGCCCCCAAAATGCTTAACCCAGACCTTGAAT 2372

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Db 2433 GGTAGAGGGTGGGCTTCAGGTCTCAACGGCTTCCCTAACACCCCTCTTCTTGCCCC 2492

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Db 2673 TGTCCATCTCAGCCCCCAGAGTATATCTGTGCTGGGAATCTCACAGAAACTCAGA 2732

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RESULT 5

AR400442

LOCUS AR400442 2904 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 703 from patent US 6620922.

ACCESSION AR400442

VERSION AR400442.1 GI:40143818

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2904)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6620922-A 703 16-SEP-2003;
FEATURES location/Qualifiers
SOURCE 1. .2904
/organisms="unknown"
/mol_type="genomic DNA"

Query Match 89.4%; Score 1916; DB 6; Length 2904;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db	2853	GAGTATATGTTTATGCTGACAAATTAAGGCTTTCTATATGTTTA	2900
RESULT 6			
AR405709			
LOCUS	AR405709	2904 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 703 from patent US 6630305.		
ACCESSION	AR405709		
VERSION	AR405709.1	GI:40154546	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2904)		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: US 6630305-A 703 07-OCT-2003;		
FEATURES	Location/Qualifiers		
Source	1..2904		
ORIGIN	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	89.4%;	Score 1916;	DB 6; Length 2904;
Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 2086;	Conservative 0;	Mismatches 1;	Indels 1; Gaps 1;
QY	57	GGCGTTCCGATGGGCAAGCCTGGGCTGTTCTGCAAGTGGCCATCTCCCTGTTCTCT	116
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Db	873	CTGTCATGAAACCGGCTGTGTCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTG	932
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QY	297	GCCTCCCTTACCAACCGGAGAAGAGGTTCCTGCCCCAATAACGAGGGGACACTGGA	356
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QY	537	GCCAGGCTGTTCGGGCGGGGCACTGCTGACCTGCGCATCTGATATGTCCTTC	596
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QY	717	CAGTAGTATTTTGACAGAGCGCACTTGCCCAATATCTCAGCGTAGAAAACTCCAGCACA	776
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QY	777	TTGGGCTGAGGGCGCTGCTCTCACTGGGTCCCAAGCTCCCGCTCTGTAGCCCCCATGGGG	836
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Db	1773	AGGAGGCCAGAAAGGCTCCATGCACTGGAATGCGGGGACTCTGACGTGATTAACCCAG	1832
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ACCESSION ARS64089
VERSION ARS64089.1 GI:53979140
KEYWORDS
SOURCE Unknown.
ORGANISM Unclasseified.
REFERENCE 1 (bases 1 to 2904)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Reter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
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JOURNAL Patent: US 6759515-A 703 06-JUL-2004;
FEATURES location/Qualifiers
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/organism="unknown"
ORIGIN /mol_type="genomic DNA"

Query Match 89.4%; Score 1916; DB 6; Length 2904;
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RESULT 8
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LOCUS Sequence 624 from Patent WO0151633.
DEFINITION AX200994
ACCESSION AX200994
VERSION AX200994.1 GI:15390821
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 624 19-JUL-2001;
CORIXA CORPORATION (US)

FEATURES
source location/Qualifiers
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Query Match 89.4%; Score 1916; DB 6; Length 2904;
Best Local Similarity 99.9%; Pred. No. 0;
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QY 57 GGGCTTCGGATGGGAGCCTGGGGCTGTTCTGACAGTGGCCATCTCCGTCTCTCT 116
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LOCUS AX267729
DEFINITION Sequence 703 from Patent WO0173032.
ACCESSION AX267729
VERSION AX267729.1 GI:16516401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0173032-A 703 04-OCT-2001;
CORIXA CORPORATION (US)
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Db 1893 TGAATAAATCACTCACTGCTTCCCATCTTAAGCCCCCTTAACCTGCACTTCTGTTA 1952
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QY 1496 GGTGGGGATCCCAACAATCAGGTCCCTGAGATAGTGTGCTATTGGGCTGATTTGC 1555
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Db 2253 GGTGGGGATCCCAACAATCAGGTCCCTGAGATAGTGTGCTATTGGGCTGATTTGC 2312
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QY 2096 GAGTATAATGTTATGTGACAAATTAAGGCTTCTTATATGTTTA 2143
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RESULT 10
AX327336 3320 bp DNA 1linear PAT 07-JAN-2002
LOCUS AX327336
DEFINITION Sequence 1 from Patent WO0181577.
ACCESSION AX327336
VERSION AX327336.1 GI:18097882
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Lau,T., Lin,R.J., Parkes,D., Parry,G., Schneider,D.W.,
Steinbrecher,R., van Heult,P.T. and Wu,J.
TITLE Dna encoding the prost 03 polypeptide
JOURNAL Patent: WO 0181577-A 1 01-NOV-2001;
SCHERING AKTIENGESELLSCHAFT (DE)
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
282..1943
/note="unnamed protein product"
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ORIGIN
Query Match 88.7%; Score 1900; DB 6; Length 3320;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2020; Conservative 0; Mismatches 0; Indels 1; Gaps 1;				
QY	1	ACCAGGGCGTGC	CCCCAGAGCTGAGCCGGGACCCGAGCCCGGAGACACTATGATGAAGCG	60
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QY	61	TTCCGATGGGCA	AGCCTGGGGCTGTTCTCTGCAAGTGC	120
Db	1243	TTCCGATGGGCA	AGCCTGGGGCTGTTCTCTGCAAGTGC	1302
QY	121	TCATGGAACGGG	CTGGTGACGATTCGGCACTCGAGCAGTCTAATTGGCCAGTGGCAG	180
Db	1303	TCATGGAACGGG	CTGGTGACGATTCGGCACTCGAGCAGTCTAATTGGCCAGTGGCAG	1362
QY	181	CTTCCCTGTGG	CTGCCGTCACATGCTCTGCCACAGTGTGCGCTGTGACAGCTT	240
Db	1363	CTTCCCTGTGG	CTGCCGTCACATGCTCTGCCACAGTGTGCGCTGTGACAGCTT	1422
QY	241	CAGCCGCGCTCA	CCGGGTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCT	300
Db	1423	CAGCCGCGCTCA	CCGGGTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCT	1482
QY	301	CCCTCTACCA	CCGGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACTGGAGGTG	360
Db	1483	CCCTCTACCA	CCGGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACTGGAGGTG	1542
QY	361	CTAGCAGTGA	GAGACAGCCTGATGACAGCTTCTCGCAGGCGCTTAAGCCTGAGCTCCCT	420
Db	1543	CTAGCAGTGA	GAGACAGCCTGATGACAGCTTCTCGCAGGCGCTTAAGCCTGAGCTCCCT	1602
QY	421	TCCCTAATGA	CACAGTGGGTGTGAGGACAGTGGCCTGTCCCACTTCCACCCGCGCTCT	480
Db	1603	TCCCTAATGA	CACAGTGGGTGTGAGGACAGTGGCCTGTCCCACTTCCACCCGCGCTCT	1662
QY	481	GCGGGCGCTCT	GCTGTGATGTCTCCGTAAGTGTGTGGTGAAGCCACCGAGGCCA	540
Db	1663	GCGGGCGCTCT	GCTGTGATGTCTCCGTAAGTGTGTGGTGAAGCCACCGAGGCCA	1722
QY	541	GGGTGGTTC	CGGGCGGCGCATCTGCTGGAACCTCGCCATCCTGGAATAGTGCCCTTCTGC	600
Db	1723	GGGTGGTTC	CGGGCGGCGCATCTGCTGGAACCTCGCCATCCTGGAATAGTGCCCTTCTGC	1782
QY	601	TGTCCAGAGT	GGCCCCATCCCTGTTAATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCA	660
Db	1783	TGTCCAGAGT	GGCCCCATCCCTGTTAATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCA	1842
QY	661	CTGCTATATG	TGTCTGCGCAGGCTGGTCTGTGCGCCATTACTTTGTCTACACAG	720
Db	1843	CTGCTATATG	TGTCTGCGCAGGCTGGTCTGTGCGCCATTACTTTGTCTACACAG	1902
QY	721	TAGTATTGA	CAAGAGCAGTTGGCCAATACTCAGCGTAGAAAACTTCCAGACATTGG	780
Db	1903	TAGTATTGA	CAAGAGCAGTTGGCCAATACTCAGCGTAGAAAACTTCCAGACATTGG	1962
QY	781	GGTGAAGG	CGCTGCTCACTGGGTCCAGCTCCCCGCTCCTGTTAGCCCCCATGGGGCTGC	840
Db	1963	GGTGAAGG	CGCTGCTCACTGGGTCCAGCTCCCCGCTCCTGTTAGCCCCCATGGGGCTGC	2022
QY	841	CGGGCTGG	CCCGCAGTTTCTGTGTGCTGCCAAAGTAATGTGGCTCTCTGTCACACCTGT	900
Db	2023	CGGGCTGG	CCCGCAGTTTCTGTGTGCTGCCAAAGTAATGTGGCTCTCTGTCACACCTGT	2082
QY	901	GCTGCTGAG	GTCGTGACAGCTGACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCCCCAG	960
Db	2083	GCTGCTGAG	GTCGTGACAGCTGACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCCCCAG	2142
QY	961	TCTCTAGG	GCTGCTGAGGCGCTTCCAAAGGGGTTTCAGTCTGAGCTTATACAGGG	1020
Db	2143	TCTCTAGG	GCTGCTGAGGCGCTTCCAAAGGGGTTTCAGTCTGAGCTTATACAGGG	2202
QY	1021	AGGCCAGA	AGGGCTCCATGACATGCAATGCG-GGGACTCTGAGGTGATTAACCAAGCTC	1079
Db	2203	AGGCCAGA	AGGGCTCCATGACATGCAATGCGGGAAGCTCTGAGGTGATTAACCAAGCTC	2262

QY	1080	AGGTTAA	CAGCTAGCCCTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGAGCTGAA	1139
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QY	1140	TAAACT	CAGTCACTGGTTTCCCATCTCTAAGCCCTTAACTGCAGCTTCGTTAATGT	1199
Db	2323	TAAACT	CAGTCACTGGTTTCCCATCTCTAAGCCCTTAACTGCAGCTTCGTTAATGT	2382
QY	1200	AGCTCT	GATGGAGTTTCTAGAGTGAACACTCTCCATGGGATTTGAACATATGAA	1259
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QY	1260	GTTATT	TTGTAGGGAGAGTCTGAGGGGCAACACACAAAGACAGGTCCCTCAGCCCA	1319
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QY	1320	CAGCACTG	CTTTTGTGATCCACCCCTCTTACCTTTTATCAGAGTGTGGCTGTTG	1379
Db	2503	CAGCACTG	CTTTTGTGATCCACCCCTCTTACCTTTTATCAGAGTGTGGCTGTTG	2562
QY	1380	GTCTTCT	GTTGCCATCAGAGACACAGGCAATTAATAATTAACTTATTATTAA	1439
Db	2563	GTCTTCT	GTTGCCATCAGAGACACAGGCAATTAATAATTAACTTATTATTAA	2622
QY	1440	AAGTAGA	AGGGAATCCATTGCTAGCTTTTCTGTGTGTGTCATAATTTGGTAGGGTG	1499
Db	2623	AAGTAGA	AGGGAATCCATTGCTAGCTTTTCTGTGTGTGTCATAATTTGGTAGGGTG	2682
QY	1500	GGGATCCC	CAACAAATCAGGTCCCCTGAGATAGCTGTGATTTGGGCTGATCTGCCAGA	1559
Db	2683	GGGATCCC	CAACAAATCAGGTCCCCTGAGATAGCTGTGATTTGGGCTGATCTGCCAGA	2742
QY	1560	ATCTTCT	TCTCTGCGGCTGTGGCCCCCAAAATGCTTAACCAAGACCTTGAATTTCTA	1619
Db	2743	ATCTTCT	TCTCTGCGGCTGTGGCCCCCAAAATGCTTAACCAAGACCTTGAATTTCTA	2802
QY	1620	CTCATCCC	AAATGATTAATTCAAATGCTGTTAACCAAGTTAGGGTGAAGGAAGTGA	1679
Db	2803	CTCATCCC	AAATGATTAATTCAAATGCTGTTAACCAAGTTAGGGTGAAGGAAGTGA	2862
QY	1680	GAGGTGG	GGCTTCAAGTCTCAAGGCTTCCCTAACCAACCCCTCTTCTTGCGCCAGCC	1739
Db	2863	GAGGTGG	GGCTTCAAGTCTCAAGGCTTCCCTAACCAACCCCTCTTCTTGCGCCAGCC	2922
QY	1740	TGTTTCCC	CCCACTTCCCTCTACTCTCTCTAGACTGGGCTGATGAAGGCACTG	1799
Db	2923	TGTTTCCC	CCCACTTCCCTCTACTCTCTCTAGACTGGGCTGATGAAGGCACTG	2982
QY	1800	CCCAAA	ATTTCCTTACCCCACTTTCCCTTACCCCACTTTCCCAACAGCTCCACA	1859
Db	2983	CCCAAA	ATTTCCTTACCCCACTTTCCCTTACCCCACTTTCCCAACAGCTCCACA	3042
QY	1860	ACCTGT	TTGGAGTACTGAGGACCAAGAACACAAAGTGCGGTTTCCCAAGCCTTGTG	1919
Db	3043	ACCTGT	TTGGAGTACTGAGGACCAAGAACACAAAGTGCGGTTTCCCAAGCCTTGTG	3102
QY	1920	CATCTCA	CCCCCAGAGTATATCTGTGCTTGGGAACTCACAAGAACTCAGAGGAC	1979
Db	3103	CATCTCA	CCCCCAGAGTATATCTGTGCTTGGGAACTCACAAGAACTCAGAGGAC	3162
QY	1980	CCCTG	CCTGAGCTAAGGAGTCTTATCTCTCAGGGGGGG 2020	
Db	3163	CCCTG	CCTGAGCTAAGGAGTCTTATCTCTCAGGGGGGG 3203	

RESULT 11
AR278711 4034 bp DNA linear PAT 10-APR-2003
LOCUS AR278711
DEFINITION Sequence 704 from patent US 6512094.
ACCESSION AR278711
VERSION AR278711.1 GI:29712957
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4034)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 704 28-JAN-2003;
FEATURES Location/Qualifiers
source 1. 4034
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Query Match 83.8%; Score 1796; DB 6; Length 4034;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 56 AGGCGTTCGGATGGGACGCTGGGGCTGTTCCCTGACATGCCCATCTCCCTGGTCTTCTC 115
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DB 2003 TCTGTCATGACCGGCTGGTGCAGCGATTCCGCACTCGAGCAGTCTATTGGCCAGTGT 2062
QY 176 GGCAGCTTCCCTGTGGTCCCGGTGCCACATGCTCTGCCACAGTGGCCGTGTGAC 235
DB 2063 GGCAGCTTCCCTGTGGTCCCGGTGCCACATGCTCTGCCACAGTGGCCGTGTGAC 2122
QY 236 AGCTTCAGCCGCGCTCAACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACT 295
DB 2123 AGCTTCAGCCGCGCTCAACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACT 2182
QY 296 GGCCTCCCTCTACCAACCGGAGAAAGCAGGTGTTCTGCCCCAAATACCGAGGGACACTGG 355
DB 2183 GGCCTCCCTCTACCAACCGGAGAAAGCAGGTGTTCTGCCCCAAATACCGAGGGACACTGG 2242
QY 356 AGGTGCTAGCAGTGAAGACAGCCTGATGACAGCTTCCCTGCAGGCCCTTAAGCCTGAGC 415
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DB 3562 AGGTAGAGGGTGGGCTTCAAGTCTCAACGGCTTCCCTAACCAACCCCTCTCTTGGCC 3621
QY 1735 CAGCTGTCTCCCCCACTTCCACTCCCTCTACTCTCTAGAGACTGGGCTGATGAAG 1794
DB 3622 CAGCTGTCTCCCCCACTTCCACTCCCTCTACTCTCTAGAGACTGGGCTGATGAAG 3681
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DB 3682 CACTGCCCAAAATTTCCCTAACCCCAACTTTCCCTAACCCCAACTTTCCCAACGCT 3741
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Db	3802	TTGTTCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAATCTCACAGAAACTCAGG	3861
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QY	2095	AGAGTATATGTTTATGTTAGTGACAAATTAAGGCTTCTTAATGTTTA	2143
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RESULT 12			
LOCUS	AR400443	4034 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 704 from patent US 6620922.		
ACCESSION	AR400443		
VERSION	AR400443.1	GI:40143820	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 4034)		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kajos,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: US 6620922-A 704 16-SEP-2003;		
FEATURES	Location/Qualifiers		
Source	1..4034 /organism="unknown" /mol_type="genomic DNA"		
ORIGIN			
Query Match	83.8%;	Score 1796;	DB 6; Length 4034;
Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 2086;	Conservative 0;	Mismatches 1;	Indels 2; Gaps 2;
QY	56	AGGCGTTTCGATGGGAGCCTGGGCTGTCTCTGAGTGGCCATCTCCCTGCTTCTC	115
Db	1943	AGGCGTTTCGATGGGAGCCTGGGCTGTCTCTGAGTGGCCATCTCCCTGCTTCTC	2002
QY	116	TCTGTGATGAGACCGGCTGTGACGATTCGGCACTCGAGAGTCTATTGGCCAGTGT	175
Db	2003	TCTGTGATGAGACCGGCTGTGACGATTCGGCACTCGAGAGTCTATTGGCCAGTGT	2062
QY	176	GGCAGCTTCCCTGTGCTGCCGCTGCACATGCTCTCCACAGTGTGGCCGTGTGAC	235
Db	2063	GGCAGCTTCCCTGTGCTGCCGCTGCACATGCTCTCCACAGTGTGGCCGTGTGAC	2122
QY	236	AGCTTCAGCCGCCCTCAACCGGGTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACT	295
Db	2123	AGCTTCAGCCGCCCTCAACCGGGTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACT	2182
QY	296	GGCTTCCTCTTACCAACCGGAGAGAGGTCTCTGCCCCAATAACGAGGGGACACTGG	355
Db	2183	GGCTTCCTCTTACCAACCGGAGAGAGGTCTCTGCCCCAATAACGAGGGGACACTGG	2242
QY	356	AGGTGCTAGCAGTGAGACAGCCTGATGACCACTTCTGTCAGGCCCTAAGCCTGAGC	415
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RESULT 13
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ACCESSION AR405710
VERSION AR405710.1 GI:40154547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 704 07-OCT-2003;
FEATURES location/Qualifiers
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DEFINITION Sequence 625 from Patent WO0151633.
ACCESSION AX200995
VERSION AX200995.1 GI:15390822
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITILE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 625 19-JUL-2001;
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Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hlc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	1916	89.4	2477	3 HSM804244	AL832933 Homo sapi
2	704	32.9	1626	9 AY407706	AY407706 Homo sapi
3	648	30.2	897	6 CA489628	CA489628 AGENCOURT
4	617	28.8	916	5 BQ950912	BQ950912 AGENCOURT
5	602	28.1	651	6 CB048223	CB048223 NISC_gj03
6	601	28.0	722	7 CN373215	CN373215 170005322
7	593	27.7	670	5 BU689021	BU689021 UI-CF-EC1
8	564	26.3	959	5 BQ950805	BQ950805 AGENCOURT
9	541	25.2	718	2 BE867241	BE867241 601442309
10	538	25.1	1025	5 BM915082	BM915082 AGENCOURT
11	528	24.6	581	7 CN373214	CN373214 170005321
12	491	22.9	589	4 BG469586	BG469586 602533622
13	475	22.2	875	5 BQ942028	BQ942028 AGENCOURT
14	474	22.1	1060	5 BM914562	BM914562 AGENCOURT
15	459	21.4	515	5 BX098291	BX098291 BX098291
16	430	20.1	437	7 CF135166	CF135166 UI-HF-CB0
17	429	20.0	734	6 CD634718	CD634718 56050152J
18	390	18.2	418	2 BF922235	BF922235 QV2-NT014
19	382	17.8	1667	5 BM912193	BM912193 AGENCOURT
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21	377	17.6	494	7 CF134970	CF134970 UI-HF-CB0
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24	339	15.8	599	6 CB050165	CB050165 NISC_gj15

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C	27	323	15.1	756	6	CD634730	CD634730 56088057J
C	28	319	14.9	448	2	BE674096	BE674096 7d74G04.x
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C	30	300	14.0	894	4	BG469520	BG469520 602532833
C	31	299	14.0	491	1	AA631143	AA631143 nq75g08.s
C	32	293	13.7	313	6	CB050330	CB050330 NISC_gj16
C	33	283	13.2	737	6	CD634720	CD634720 56050236J
C	34	282	13.2	586	5	BP326798	BP326798 BP326798
C	35	281	13.1	469	1	AI703348	AI703348 wd93b09.x
C	36	275	12.8	1450	9	AY407707	AY407707 Pan trogl
C	37	270	12.6	325	2	BE673709	BE673709 7d79G07.x
C	38	268	12.5	327	1	AI969820	AI969820 wq75C01.x
C	39	266	12.4	716	6	CD634717	CD634717 56050152H
C	40	265	12.4	435	6	CB049513	CB049513 NISC_gj11
C	41	264	12.3	320	2	BF223229	BF223229 7p51C08.x
C	42	263	12.3	315	1	AA640153	AA640153 mp28D03.s
C	43	261	12.2	320	2	BF223843	BF223843 7q80D09.x
C	44	260	12.1	313	1	AI587483	AI587483 tr51C10.x
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ALIGNMENTS

RESULT 1
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DEFINITION AL832933
ACCESSION AL832933
VERSION AL832933.1 GI:21733520
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (Bases 1 to 2477)
Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Well,B., Amlid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

CONSRMT
TITLE The German cDNA Consortium
JOURNAL Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.

This clone (DKFZp666D0110) is available at the RZPD Deutsches
Reisourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp666D0110
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

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Query Match 89.4%; Score 1916; DB 3; Length 2477;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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OY 117 CTGGTCATGACCGGCTGGTGCAGCGATTGGCACTCGAGCAGTCTATTGGCCAGTGTG 176
Db 421 CTGGTCATGACCGGCTGGTGCAGCGATTGGCACTCGAGCAGTCTATTGGCCAGTGTG 480
OY 177 GCAGCTTTCCTGTGCTGCCGGTGCACATGCTCTGCCACAGTGTGCGCTGTGACA 236
Db 481 GCAGCTTTCCTGTGCTGCCGGTGCACATGCTCTGCCACAGTGTGCGCTGTGACA 540
OY 237 GCTTACAGCCGCTTCAACGGGTTCACTTCTCAGCCCTGACAGATCTGCTTACACACTG 296
Db 541 GCTTACAGCCGCTTCAACGGGTTCACTTCTCAGCCCTGACAGATCTGCTTACACACTG 600
OY 297 GCCTCCCTCTACCAACGGGAGAACAGGTGTCTCTGCCAATAACGAGGGGACACTGA 356
Db 601 GCCTCCCTCTACCAACGGGAGAACAGGTGTCTCTGCCAATAACGAGGGGACACTGA 660
OY 357 GGTGCTAGCAGTGAAGACAGCTGTATGACAGCTTCTGCCAGGCTTAAAGCTGAGCT 416
Db 661 GGTGCTAGCAGTGAAGACAGCTGTATGACAGCTTCTGCCAGGCTTAAAGCTGAGCT 720
OY 417 CCCTTCCCTAATGACACAGTGGGTGTGAGGACAGTGGCTGTCCCACTCCACCCGCG 476
Db 721 CCCTTCCCTAATGACACAGTGGGTGTGAGGACAGTGGCTGTCCCACTCCACCCGCG 780
OY 477 CTCTGCGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGGGTGAGCCCAACCGAG 536
Db 781 CTCTGCGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGGGTGAGCCCAACCGAG 840
OY 537 GCCAGGGGTTCGGGGCCGGGCACTGCTGGAACCTCGCCATCTTGATAGTGCCTTC 596
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Db 901 CTGCTGTCCAGGTGGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCT 960
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OY 1496 GGTGGGGATCCCAACAATCAGTCCCTGAGATAGCTGTGATTTGGCTGATCATTTGC 1555
Db 1801 GGTGGGGATCCCAACAATCAGTCCCTGAGATAGCTGTGATTTGGCTGATCATTTGC 1860
OY 1556 CAGATCTTCTCTCTGCGGGCTGCGCCCCCAAAATGCTTAAACCCAGAACCTTGAAT 1615
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OY 1616 TCTACTCATCCCAAATGATAATTCCAAATGCTGTTAACCCAAAGTTAGGTGTGAAGAA 1675
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OY 1916 TGTCACTCAGCCCCCAGAGTATCTGTGCTTGGGGAATCTCACAGAACTCAGGA 1975
Db 2221 TGTCACTCAGCCCCCAGAGTATCTGTGCTTGGGGAATCTCACAGAACTCAGGA 2280
OY 1976 GCACCCCTGCTGAGCTAAGGAGGTTTATCTCTCAGGGGGGTTTAAGTGCCGTTTG 2035
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Db	2401	GAGTATATGTTTATGTTGACAAATTTAAAGGCTTCTTATATGTTTA	2448
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LOCUS			linear
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ACCESSION	AY407706	genomic survey sequence.	
VERSION			
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SOURCE	GSS.		
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	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1	(bases 1 to 1626)	
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,		
	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,		
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
	Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous		
	gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2	(bases 1 to 1626)	
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,		
	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,		
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
	Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,		
	Rockville, MD 20850, USA		
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QY	298	CCTCCCTCTACCAACCGGAGAGCAGGTGTTCTCTGCCCCAAATACCGAGGGGACACTGGAG	357
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		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 897)			
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/.			
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL		Unpublished (1999)			
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgaphs-romail.nih.gov Tissue Procurement: Kristi A. Eglund, Ira Pastan CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov plate: L1AM14284 row: e column: 18 High quality sequence stop: 625.			
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		Directionally cloned. Priming method: oligo-dT. Average			
		insert size: 1800 bp. Library amplification: 26,000 fold.			
		Kristi A. Eglund, James J. Vincent, Robert Strausberg,			
		Bungkok Uee & Ira Pastan: Discovery of new breast			

ORIGIN

cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

Query Match 30.2%; Score 648; DB 6; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 601 TGTCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCA 648
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RESULT 4
BQ950912 916 bp mRNA linear EST 21-AUG-2002
LOCUS BQ950912 916 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT 8754471 Lupski sciatic nerve Homo sapiens cDNA clone
IMAGE:6205362 5', mRNA sequence.
ACCESSION BQ950912
VERSION BQ950912.1 GI:22366390
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13628 row: b column: 19
High quality sequence stop: 579.

FEATURES

source
1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6205362"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_1lb="Lupski sciatic nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCCG-3' and
5'-GACTAGTCTAGATCGAGCGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

Query Match 28.8%; Score 617; DB 5; Length 916;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 TAGCCTCTAGTGAAGACACAGCTAGAGAGGGTTTGGAGCTGAATAACTCAGTCA 1151
Db 1 TAGCCTCTAGTGAAGACACAGCTAGAGAGGGTTTGGAGCTGAATAACTCAGTCA 60
QY 1152 CCTGTTTCCCATCTTAAGCCCTTAACCTGCAGCTTCTGTTAATGATCTTGATG 1211
Db 61 CCTGTTTCCCATCTTAAGCCCTTAACCTGCAGCTTCTGTTAATGATCTTGATG 120
QY 1212 GGAGTTTCTAGATGAACACACTCCCTCATGGGATTGAAACATATGAAGTATTGTAGG 1271
Db 121 GGAGTTTCTAGATGAACACACTCCCTCATGGGATTGAAACATATGAAGTATTGTAGG 180
QY 1272 GGAAGAGTCTTGAAGGGGCAACACAGAGTCCCTCAGCCCAAGCAGTGTCTT 1331
Db 181 GGAAGAGTCTTGAAGGGGCAACACAGAGTCCCTCAGCCCAAGCAGTGTCTT 240
QY 1332 TTTGCTGATCCACCCCTCTTACCTTTTATCAGAGATGCGCTGTGCTCTCTGTTG 1391
Db 241 TTTGCTGATCCACCCCTCTTACCTTTTATCAGAGATGCGCTGTGCTCTCTGTTG 300
QY 1392 CCATCAGAGACACAGGCAATTAATTTAATTTAATTTAACAAGTAGAAGGA 1451
Db 301 CCATCAGAGACACAGGCAATTAATTTAATTTAATTTAACAAGTAGAAGGA 360
QY 1452 ATCCATGCTAGCTTTTCTGTGTGTGCTCTAATATTTGGGTAGGGTGGGATCCCA 1511
Db 361 ATCCATGCTAGCTTTTCTGTGTGTGCTCTAATATTTGGGTAGGGTGGGATCCCA 420
QY 1512 CAATCAGTCCCTGAGATAGCTGTCATTGGCTGATTCATGCGAATCTTCTTCC 1571
Db 421 CAATCAGTCCCTGAGATAGCTGTCATTGGCTGATTCATGCGAATCTTCTTCC 480
QY 1572 TGGGCTGTGGCCCCCAAAATGCTTAACCCAGAGACTTGAATTTCTACTCATCCAAAT 1631
Db 481 TGGGCTGTGGCCCCCAAAATGCTTAACCCAGAGACTTGAATTTCTACTCATCCAAAT 540
QY 1632 GATAATTCCAATGCTGTTAACCCAGGTTAGGCTGTGAAGAGTAGAGGCTGGGCT 1691
Db 541 GATAATTCCAATGCTGTTAACCCAGGTTAGGCTGTGAAGAGTAGAGGCTGGGCT 600


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Qy 1692 TCAGGTCACAGGCTT 1708
Db 601 TCAGGTCACAGGCTT 617

RESULT 5
LOCUS CB048223
DEFINITION NISC_gj03e11.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3270644
5', mRNA sequence.
ACCESSION CB048223
VERSION CB048223
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS 1 (bases 1 to 651)
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
info@image.lnl.gov
Plate: LLM8006 row: J column: 21
Seq primer: M13RPI reverse primer (ABI).
FEATURES
Source
1. .651
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3270644"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP_Pr22 was prepared, and as
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
```

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Db 194 ATAATCCAAATGCTGTTACCCAAAGTTAGGCTTGAAGAGTAGAGGTGGGCTT 253
Qy 1693 CAGGTCACACGGCTTCCCTAACCAACCCCTCTTCTCTGGCCAGCCTGGTTCACCCAC 1752
Db 254 CAGGTCACACGGCTTCCCTAACCAACCCCTCTTCTCTGGCCAGCCTGGTTCACCCAC 313
Qy 1753 TTCCACTCCCTCTACTCTCTCTAGAGCTGGGCTGATGAAGGCACTGCCAAATTTC 1812
Db 314 TTCCACTCCCTCTACTCTCTCTAGAGCTGGGCTGATGAAGGCACTGCCAAATTTC 373
Qy 1813 CTACCCCAACTTTCCCTTACCCCACTTTCCCACTGCTCCCACTCAACCCCTGTTGAG 1872
Db 374 CTACCCCAACTTTCCCTTACCCCACTTTCCCACTGCTCCCACTCAACCCCTGTTGAG 433
Qy 1873 CTACTGCAGACCAAGACCAAGTGCCTTTCCCAAGCCTTGTCCATCTCAGCCCC 1932
Db 434 CTACTGCAGACCAAGACCAAGTGCCTTTCCCAAGCCTTGTCCATCTCAGCCCC 493
Qy 1933 AGAGTATATCTGTGCTTGGGAATCTCACACAGAACTCAGAGCAACCCCTGCTGAGC 1992
Db 494 AGAGTATATCTGTGCTTGGGAATCTCACACAGAACTCAGAGCAACCCCTGCTGAGC 553
Qy 1993 TAAGGAGGCTTATCTCTCAGGGGGGTTTAAGTGCCTTTGCAATATATGCTTAT 2052
Db 554 TAAGGAGGCTTATCTCTCAGGGGGGTTTAAGTGCCTTTGCAATATATGCTTAT 613
Qy 2053 TT 2054
Db 614 TT 615

RESULT 6
LOCUS CN373215 722 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000532237472 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN373215
VERSION CN373215.1 GI:47373149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 722)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 722 Std Error: 0.00.
FEATURES
Source
1. .722
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_lib="GRN ES"
/note="Oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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Query Match 28.0%; Score 601; DB 7; Length 722;
Best Local Similarity 99.9%; Pred. No. 1.9e-313;
Matches 721; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 751 ACTCAGCGTAGAAAACTTCCAGACATTTGGGGTGAGGGGCTGCTCACTGGGTCCAGC 810
Db 1 ACTCAGCGTAGAAAACTTCCAGACATTTGGGGTGAGGGGCTGCTCACTGGGTCCAGC 60
QY 811 TCCCCGCTCTGTAGTACCCCAAGGGGCTGCCGGGCTGGCCGAGTTTCTGTGTGCCA 870
Db 61 TCCCCGCTCTGTAGTACCCCAAGGGGCTGCCGGGCTGGCCGAGTTTCTGTGTGCCA 120
QY 871 AAGTAATGTGGCTCTCTGCTGCCACCTGTGCTGCTGAGGTGCGTAGCTGCACAGCTGGG 930
Db 121 AAGTAATGTGGCTCTCTGCTGCCACCTGTGCTGCTGAGGTGCGTAGCTGCACAGCTGGG 180
QY 931 GGCTGGGGCGTCCCT 990
Db 181 GGCTGGGGCGTCCCT 240
QY 991 AAGGGGGTTTCAGTCTGACTTATACAGGAGGCCAGAGGGGCTCCATGCACCTGGAATGC 1050
Db 241 AAGGGGGTTTCAGTCTGACTTATACAGGAGGCCAGAGGGGCTCCATGCACCTGGAATGC 300
QY 1051 -GGGACTCTGACGTGATTAACCCAGGCTCAGGGTTAAACAGCTAGCCTCTAGTTGAGAC 1109
Db 301 GGGGACTCTGACGTGATTAACCCAGGCTCAGGGTTAAACAGCTAGCCTCTAGTTGAGAC 360
QY 1110 ACACCTAGAGAGGGTTTGGGAGCTGAATAAATCACTCAGTCACTGGTTCCCATCTCTA 1169
Db 361 ACACCTAGAGAGGGTTTGGGAGCTGAATAAATCACTCAGTCACTGGTTCCCATCTCTA 420
QY 1170 AGCCCTTAACCTGACGCTTCTGTTAATGATGCTCTGTCATGGAGTTCTAGATGAAA 1229
Db 421 AGCCCTTAACCTGACGCTTCTGTTAATGATGCTCTGTCATGGAGTTCTAGATGAAA 480
QY 1230 CACTCCTCCATGGGATTTGAACATATGAAGTTATTGTAGGGGAAGTCTGAGGGGC 1289
Db 481 CACTCCTCCATGGGATTTGAACATATGAAGTTATTGTAGGGGAAGTCTGAGGGGC 540
QY 1290 AACACACAGAGAGGCTCCCTCAGCCCAAGCACTGCTTTTGGTGTATCCACCCGCC 1349
Db 541 AACACACAGAGAGGCTCCCTCAGCCCAAGCACTGCTTTTGGTGTATCCACCCGCC 600
QY 1350 TCTTACCTTTTATCAGGATGTGGCCTGTGGCTCTTCTGTGTCATCAAGAGACAGG 1409
Db 601 TCTTACCTTTTATCAGGATGTGGCCTGTGGCTCTTCTGTGTCATCAAGAGACAGG 660
QY 1410 CATTAAATATTTAATTATTATTAAAGTAGAGGGAATCATGTGCTAGCTTTTC 1469
Db 661 CATTAAATATTTAATTATTATTAAAGTAGAGGGAATCATGTGCTAGCTTTTC 720
QY 1470 TG 1471
Db 721 TG 722

RESULT 7
BU689021/c 670 bp mRNA linear EST 07-OCT-2002
LOCUS UI-CF-EC1-ady-f-04-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
DEFINITION UI-CF-EC1-ady-f-04-0-UI 3', mRNA sequence.
ACCESSION BU689021
VERSION BU689021.1 GI:23546376
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 670)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548

COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-28, >At rich#low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
location/Qualifiers
1..670
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-ady-f-04-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1lb="UI-CF-EC1"
/note="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p77T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTCTTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTCTTAC"

ORIGIN
Query Match 27.7%; Score 593; DB 5; Length 670;
Best Local Similarity 99.8%; Pred. No. 4.9e-309;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1500 GGGATCCCAACAATCAGTCCCTGAGATAGCTGTGATGGGCTGATCATTGCCAGA 1559
Db 661 GGGATCCCAACAATCAGTCCCTGAGATAGCTGTGATGGGCTGATCATTGCCAGA 602
QY 1560 ATCTTCTTCTCTGGGGTCTGGCCCAAAATGCTTAACCAAGACCTTGAATTTCTA 1619
Db 601 ATCTTCTTCTCTGGGGTCTGGCCCAAAATGCTTAACCAAGACCTTGAATTTCTA 542
QY 1620 CTCATCCCAATGATAATTCGAATGCTGTACCCCAAGTTAGGGTGTGAAGGAAGTA 1679
Db 541 CTCATCCCAATGATAATTCGAATGCTGTACCCCAAGTTAGGGTGTGAAGGAAGTA 482
QY 1680 GAGGTTGGGCTTCAGGTTCAAGGCTTCCCTTAACCAAGGCTTCTTCTGGCCAGCC 1739
Db 481 GAGGTTGGGCTTCAGGTTCAAGGCTTCCCTTAACCAAGGCTTCTTCTGGCCAGCC 422
QY 1740 TGGTCCCCCACTTCCACTCCCTCTACTCTCTCTAGAGCTGGGCTGATGAAGCACTG 1799
Db 421 TGGTCCCCCACTTCCACTCCCTCTACTCTCTCTAGAGCTGGGCTGATGAAGCACTG 362

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QY 1800 CCCAAATTTCCCTACCCCAACTTTCCCTACCCCAACTTTCCCAAGCTCCACA 1859
Db 361 CCCAAATTTCCCTACCCCAACTTTCCCTACCCCAACTTTCCCAAGCTCCACA 302
QY 1860 ACCCTGTTTGAGACTACTGCAGAGCAGACACAAGTGCCTTTCCCAAGCTTGTG 1919
Db 301 ACCCTGTTTGAGACTACTGCAGAGCAGACACAAGTGCCTTTCCCAAGCTTGTG 242
QY 1920 CATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAATCTCACACAGAACTCAGAGC 1979
Db 241 CATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAATCTCACACAGAACTCAGAGC 182
QY 1980 CCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAAGTCCGTTGCAAT 2039
Db 181 CCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAAGTCCGTTGCAAT 122
QY 2040 AATGTCGTCTTATTTTTCAGCGGGGTAATTTTATACCTGTAAGTGAATCAGAGT 2099
Db 121 AATGTCGTCTTATTTTTCAGCGGGGTAATTTTATACCTGTAAGTGAATCAGAGT 62
QY 2100 AATAATTTATGTTGACAAATTAAGCTTTCTTATATGTTTA 2143
Db 61 AATAATTTATGTTGACAAATTAAGCTTTCTTATATGTTTA 18

RESULT 8
LOCUS BQ950805 959 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204253 5', mRNA sequence.
ACCESSION BQ950805
VERSION BQ950805.1 GI:22366283
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13625 row: d column: 14
High quality sequence start: 2
High quality sequence stop: 490.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204253"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCG-3' and
5'-GACTAGTTCTAGATCGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life

```

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ORIGIN
Technology. "
Query Match 26.3%; Score 564; DB 5; Length 959;
Best Local Similarity 100.0%; Pred. No. 2.6e-293;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 CGTGGGTGCTGAGAGGAGTGGGCTGCTCCACCTCCACCCGGGCTTGCGGGCTTGC 493
Db 7 CGTGGGTGCTGAGAGGAGTGGGCTGCTCCACCTCCACCCGGGCTTGCGGGCTTGC 66
QY 494 CTGTGATGTCCTCCGTACGTGTGTGGTGGGTGAGCCCAAGGAGGAGGTGTTCCGGG 553
Db 67 CTGTGATGTCCTCCGTACGTGTGTGGTGGGTGAGCCCAAGGAGGAGGTGTTCCGGG 126
QY 554 CCGGGGATCTGCTGAGCCTGCGCATCTTGATAGTGCCTTCTGCTGCCAGGTGC 613
Db 127 CCGGGGATCTGCTGAGCCTGCGCATCTTGATAGTGCCTTCTGCTGCCAGGTGC 186
QY 614 CCATCCCTGTTTATGGGCTCCATGTCAGCTCAGCCAGTCTGTCATGCTATATGTT 673
Db 187 CCATCCCTGTTTATGGGCTCCATGTCAGCTCAGCCAGTCTGTCATGCTATATGTT 246
QY 674 GTCTGCCAGAGCCTGGGTGCTGCTGCCATTACTTTGCTACAGAGTAGTATTGACAA 733
Db 247 GTCTGCCAGAGCCTGGGTGCTGCTGCCATTACTTTGCTACAGAGTAGTATTGACAA 306
QY 734 GAGGAGCTTGCCCAATATCTCAGCGTAGAAACTTCCAGACATTGGGGTGAGGCGCTG 793
Db 307 GAGGAGCTTGCCCAATATCTCAGCGTAGAAACTTCCAGACATTGGGGTGAGGCGCTG 366
QY 794 CCTCACTGGGTGCCAGCTCCCGCTCTGTTAGCCCCATGGGGCTGCCGGGCTGCCGCC 853
Db 367 CCTCACTGGGTGCCAGCTCCCGCTCTGTTAGCCCCATGGGGCTGCCGGGCTGCCGCC 426
QY 854 AGTTTCTGTGCTGCTGCCAAAGTAATGTGGCTCTGTGCTGCCACCTGTGCTGAGGTGC 913
Db 427 AGTTTCTGTGCTGCTGCCAAAGTAATGTGGCTCTGTGCTGCCACCTGTGCTGAGGTGC 486
QY 914 GTAGCTCACAGCTGGGGGCTGGGCGTCCCTCTCTCTCTCCCAAGTCTCTAGGGCTGC 973
Db 487 GTAGCTCACAGCTGGGGGCTGGGCGTCCCTCTCTCTCTCCCAAGTCTCTAGGGCTGC 546
QY 974 CTGACTGAGAGCCTTCCAAAGGGG 997
Db 547 CTGACTGAGAGCCTTCCAAAGGGG 570

RESULT 9
LOCUS BE867241 718 bp mRNA linear EST 20-OCT-2000
DEFINITION 601442309F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846411 5',
IMAGE:3846411 5', mRNA sequence.
ACCESSION BE867241
VERSION BE867241.1 GI:10316017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

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Plate: LLAM9559 row: a column: 04
High quality sequence stop: 693.

FEATURES

Source

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1. .718
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3846411"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH MGC_65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "

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ORIGIN

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Query Match      25.2%; Score 541; DB 2; Length 718;
Best Local Similarity 100.0%; Pred. No. 7.6e-281;
Matches 541; Conservative 0; Mismatches 0; Indels 0. Gaps 0.
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QY	116	TCTGTCATGACCGCGCTGCTGACGCGATTGCGCACTGACGAGCTTATTGGCCAGTGT	175
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QY	176	GGCAGCTTTCCCTGTGGCTGCCGGGTGCCACATGCTGTGCCACAGTGTGGCCGTGTAC	235
Db	61	GGCAGCTTTCCCTGTGGCTGCCGGGTGCCACATGCTGTGCCACAGTGTGGCCGTGTAC	120
QY	236	AGCTTCAGCCGCGCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACT	295
Db	121	AGCTTCAGCCGCGCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACT	180
QY	296	GGCCTCCCTTACCAACCGGGAGAAGCAGGTGTTCTGCCCAATACCGAGGGGCACTGG	355
Db	181	GGCCTCCCTTACCAACCGGGAGAAGCAGGTGTTCTGCCCAATACCGAGGGGCACTGG	240
QY	356	AGGTGTAGCAGTAGAGCACAGCCTGATGACCACTTCTGCCAGGCCCTAAAGCTTGAGC	415
Db	241	AGGTGTAGCAGTAGAGCACAGCCTGATGACCACTTCTGCCAGGCCCTAAAGCTTGAGC	300
QY	416	TCCCTTCCCTAATGACACAGTGGGTGCTGAGGCGAGTGGCCTGCTCCACCTCCACCCGC	475
Db	301	TCCCTTCCCTAATGACACAGTGGGTGCTGAGGCGAGTGGCCTGCTCCACCTCCACCCGC	360
QY	476	GCTCTGCGGGGCTCTGCCTGTGATGTCTCCGTAAGTGTGTGTGTGAGAGCCACCGA	535
Db	361	GCTCTGCGGGGCTCTGCCTGTGATGTCTCCGTAAGTGTGTGTGTGAGAGCCACCGA	420
QY	536	GGCCAGGGTGTTCGCGGCGCGGGCACTGCTGAGACCTGCGCCATCTGAGTAGTGCCTT	595
Db	421	GGCCAGGGTGTTCGCGGCGCGGGCACTGCTGAGACCTGCGCCATCTGAGTAGTGCCTT	480
QY	596	CCTGCTGTCCCAAGTGGGCCCACTCCTGTATTATGGGCTCCATTTGTCAGCTCAGCCAGTC	655
Db	481	CCTGCTGTCCCAAGTGGGCCCACTCCTGTATTATGGGCTCCATTTGTCAGCTCAGCCAGTC	540
QY	656	T 656	
Db	541	T 541	

RESULT 10	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BM915082							
BM915082	1025 bp	mRNA	linear	EST 12-MAR-2002			
AGENCOURT_6702317	NIH_MGC_41	Homo sapiens	CDNA clone	IMAGE:5481218			
5', mRNA	Sequence.						
BM915082							
BM915082.1	GI:19365461						
EST.							
Homo sapiens	(human)						
Homo sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							

REFERENCE	1 (bases 1 to 1025)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

COMMENT

Plate: LLCM2005 row: f column: 03
High quality sequence start: 35
High quality sequence stop: 657.

FEATURES

Source

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1. 1025
location/gene/1025
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5481218"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NINH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NINH MGC library."

```

ORIGIN

Query Match	25.14;	Score 538;	DB 5;	length 1025;
Best Local Similarity	99.6%;	Pred. No. 3.3e-279;		
Matches 758; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1.

QY	615	CCATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGCTGTGCATCTGCCTATATG	674
Db	12	CCATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGCTGTGCATCTGCCTATATG	71
QY	675	TCGCGCGCAGGCTGGGCTGGTGCATTTACTTTGCTACAGAGTAGTATTTGACAAG	734
Db	72	TCGCGCGCAGGCTGGGCTGGTGCATTTACTTTGCTACAGAGTAGTATTTGACAAG	131
QY	735	AGGCACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGACAATTGGGGTGGAGGCTGC	794
Db	132	AGGCACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGACAATTGGGGTGGAGGCTGC	191
QY	795	CTCAGCTGGGTCCCGAGCTCCCGCTCCTGTGTAGCCCCATGGGGCTGCCGGCTGCCCA	854
Db	192	CTCAGCTGGGTCCCGAGCTCCCGCTCCTGTGTAGCCCCATGGGGCTGCCGGCTGCCCA	251
QY	855	GTTTCTGTGTGCTGCCAAAGTAATGTGGCTCTGTGTCGCCACCTGTGCTGAGGTGC	914
Db	252	GTTTCTGTGTGCTGCCAAAGTAATGTGGCTCTGTGTCGCCACCTGTGCTGAGGTGC	311
QY	915	TAGCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCTCCAGTCTTAGGGCTGCC	974
Db	312	TAGCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCTCCAGTCTTAGGGCTGCC	371
QY	975	TGACTGGAGGCCCTTCCAAAGGGGGTTTCACTGTGACTTATACAGGAGGCCAAGGGCT	1034
Db	372	TGACTGGAGGCCCTTCCAAAGGGGGTTTCACTGTGACTTATACAGGAGGCCAAGGGCT	431
QY	1035	CCATGCACCTGGAATGC-GGGACTCTGCAGGTGATTAACCAGGCTCAGGGTTAACGCTA	1093
Db	432	CCATGCACCTGGAATGC-GGGGACTCTGCAGGTGATTAACCAGGCTCAGGGTTAACGCTA	491
QY	1094	GCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTGGAGCTGAATTAACCTCAGTACC	1153

Db 492 GCCTCTAGTGTGAGACACACCTAGAGAGGGTTTGGAGCTGAATAAAGTCACTCACC 551

Qy 1154 TGGTTTCCCATCTCTAAGCCCCCTTAACTGACGCTTGGTTAATGAGCTCTTGATGGG 1213

Db 552 TGGTTTCCCATCTCTAAGCCCCCTTAACTGACGCTTGGTTAATGAGCTCTTGATGGG 611

Qy 1214 AGTTTCTAGATGAACACTCTCCATGGGATTGACATATGAAGTTATTTGTAGGGG 1273

Db 612 AGTTTCTAGATGAACACTCTCCATGGGATTGACATATGAAGTTATTTGTAGGGG 671

Qy 1274 AAGAGTCTGAGGGGCAACACAGAACCAAGTCCCTCAGCCCAAGCACTGTCTTT 1333

Db 672 AAGAGTCTGAGGGGCAACACAGAACCAAGTCCCTCAGCCCAAGCACTGTCTTT 731

Qy 1334 TGGTGTCCACCCCCCTTACCTTTATCAGGATGTGCC 1374

Db 732 TGGTGTCCACCCCCCTTACCTTTATCAGGATGTGCC 772

RESULT 11

CN373214 581 bp mRNA linear EST 16-MAY-2004

LOCUS 1700532189001 GRN_ES Homo sapiens cDNA 5', mRNA sequence.

DEFINITION CN373214

ACCESSION CN373214

VERSION CN373214.1 GI:47373148

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 581)

AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. W.

TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 581 Std Error: 0.00.

FEATURES

Source

1. 581

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"

/clone_lib="GRN ES"

/note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 24.6%; Score 528; DB 7; Length 581;

Best Local Similarity 100.0%; Pred. No. 8.3e-274;

Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 CTTGGTTCCCATCTCTAAGCCCCCTTAACTGACGCTTGGTTAATGAGCTCTTGATG 1211

Db 39 CTTGGTTCCCATCTCTAAGCCCCCTTAACTGACGCTTGGTTAATGAGCTCTTGATG 98

Qy 1212 GGAATTTCTAGATGAACACTCTCTCCATGGGATTGAACATATGAAGTTATTTGTAGG 1271

Db 99 GGAATTTCTAGATGAACACTCTCTCCATGGGATTGAACATATGAAGTTATTTGTAGG 158

Qy 1272 GGAAGAGTCTGAGGGGCAACACAGAACCAAGTCCCTCAGCCCAAGCACTGTCTT 1331

Db 159 GGAAGAGTCTGAGGGGCAACACAGAACCAAGTCCCTCAGCCCAAGCACTGTCTT 218

Qy 1332 TTGCTGATCCACCCCCCTTACCTTTTATCAGGATGTGGCTGTGCTCTGTTG 1391

Db 219 TTGCTGATCCACCCCCCTTACCTTTTATCAGGATGTGGCTGTGCTCTGTTG 278

Qy 1392 CCATCAGAGACACAGGCATTAAATTTAACTTATTATTAAACAAGTAGAAGGA 1451

Db 279 CCATCAGAGACACAGGCATTAAATTTAACTTATTATTAAACAAGTAGAAGGA 338

Qy 1452 ATCATGCTAGCTTTTCTGTGTGTGTCTAATATTGGGATGGGATCCCCAA 1511

Db 339 ATCATGCTAGCTTTTCTGTGTGTGTCTAATATTGGGATGGGATCCCCAA 398

Qy 1512 CAATCAGTCCCTGAGATAGCTGTCATTGGGCTGATCATTCAGAACTCTCTCC 1571

Db 399 CAATCAGTCCCTGAGATAGCTGTCATTGGGCTGATCATTCAGAACTCTCTCC 458

Qy 1572 TGGGCTGCGCCCCCAAAATGCTTAACCCAGACCTTGAAATTCTACTCATCCAAAT 1631

Db 459 TGGGCTGCGCCCCCAAAATGCTTAACCCAGACCTTGAAATTCTACTCATCCAAAT 518

Qy 1632 GATTAATCCAAATGCTGTATCCCAAGGTTAGGCTGTGAAGGAAGTA 1679

Db 519 GATTAATCCAAATGCTGTATCCCAAGGTTAGGCTGTGAAGGAAGTA 566

RESULT 12

BG469586 589 bp mRNA linear EST 21-MAR-2001

LOCUS 602533622F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661500 5', mRNA sequence.

DEFINITION BG469586

ACCESSION BG469586

VERSION BG469586.1 GI:13401861

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 589)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA library Preparation: Ling Hong/Rubin Laboratory

cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov

Plate: LNCM1460 row: k column: 05

High quality sequence stop: 587.

FEATURES

Source

1. 589

Location/Qualifiers

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/clone_lib="NIH MGC 15"

/note="Organ: colon; Vector: pOTB7; site 1: XhoI; site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM2002 row: m column: 14
High quality sequence stop: 485.

FEATURES

Source

location/Qualifiers

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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 22.1%; Score 474; DB 5; Length 1060;
Matches 474; Conservativity 100.0%; Pred. No. 1.6e-244;
Mismatch 0; Indels 0; Gaps 0;

QY 352 CTGAGGTGCTAGCAGTGAGGACAGCTTGATGACCAAGCTTCCGCGAGCCCTAAGCCTG 411
Db 1 CTGAGGTGCTAGCAGTGAGGACAGCTTGATGACCAAGCTTCCGCGAGCCCTAAGCCTG 60
QY 412 GAGCTCCCTTCCCTAATGAGACACGTGGGTGCTGGAGGACAGTGGCTGCTCCACCTCCAC 471
Db 61 GAGCTCCCTTCCCTAATGAGACACGTGGGTGCTGGAGGACAGTGGCTGCTCCACCTCCAC 120
QY 472 CCGCGCTGCGGGGCTCTGCTGATGTCTCCGTACGTGTGGTGGTGAGGCCA 531
Db 121 CCGCGCTGCGGGGCTCTGCTGATGTCTCCGTACGTGTGGTGGTGAGGCCA 180
QY 532 CCGAGGCCAGGGTGTCCGGGCGGGGCATCTGCCTGAGCCTGCATCCTGATAGTG 591
Db 181 CCGAGGCCAGGGTGTCCGGGCGGGGCATCTGCCTGAGCCTGCATCCTGATAGTG 240
QY 592 CCTTCTGCTGTCCAGGTGGGCCCATCCCTGTTATGGGGCTCCATGTCCAGCTCAGCC 651
Db 241 CCTTCTGCTGTCCAGGTGGGCCCATCCCTGTTATGGGGCTCCATGTCCAGCTCAGCC 300
QY 652 AGTCTGTCACTGCCTATATGTGTCTGCGGACAGGCTGGGTCTGTGCCATTACTTGG 711
Db 301 AGTCTGTCACTGCCTATATGTGTGTCTGCGGACAGGCTGGGTCTGTGCCATTACTTGG 360
QY 712 CTACACAGGTAGTATTGACAAGAGCACTTGCCAAATACTCAGGTAGAAACTTCCA 771
Db 361 CTACACAGGTAGTATTGACAAGAGCACTTGCCAAATACTCAGGTAGAAACTTCCA 420
QY 772 GCACATTGGGGTGAGGGCTGCTCACTGGGTGCCAGCTCCCGCTCCTGTTA 825
Db 421 GCACATTGGGGTGAGGGCTGCTCACTGGGTGCCAGCTCCCGCTCCTGTTA 474

RESULT 15
LOCUS BX098291 515 bp mRNA linear EST 04-FEB-2003
DEFINITION BX098291 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE98P04693 ; IMAGE:308595, mRNA sequence.
ACCESSION BX098291
VERSION BX098291.1 GI:27843586
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 515)

AUTHORS

Ebert, L., Heil, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.

TITLE

Human Unigeneset - RZPD3

JOURNAL

Unpublished (2003)

COMMENT

Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE98P04693.
RZPDLIB; I.M.A.G.E. cDNA clone collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972> Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCAACACAGAAACAGCTATGAC.

FEATURES

source

1..515
/organism="Homo sapiens"
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modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGGAGGTGAGGGCTTCAGGTCTCAACGGCTTCCCTAAC
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

ORIGIN

Query Match

Best Local Similarity 21.4%; Score 459; DB 5; Length 515;
Matches 459; Conservativity 100.0%; Pred. No. 2.1e-236;
Mismatch 0; Indels 0; Gaps 0;

QY 1596 TAACCCAGACCTTGAAATTTACTCATCCCAATGATTAATTCAAATGCTGTACCCA 1655
Db 34 TAACCCAGACCTTGAAATTTACTCATCCCAATGATTAATTCAAATGCTGTACCCA 93
QY 1656 AGGTAGGGTGTGAAGGAGGTGAGGGCTTCAGGTCTCAACGGCTTCCCTAAC 1715
Db 94 AGGTAGGGTGTGAAGGAGGTGAGGGCTTCAGGTCTCAACGGCTTCCCTAAC 153
QY 1716 CACCCCTCTTCTTGCCCAAGCTGTGTCCTCCCACTTCCACTCCCTCTACTCTCT 1775
Db 154 CACCCCTCTTCTTGCCCAAGCTGTGTCCTCCCACTTCCACTCCCTCTACTCTCT 213
QY 1776 AGGACTGGCTGATGAAGGACATGCCAAATTTCCCTACCCCACTTCCCTACCC 1835
Db 214 AGGACTGGCTGATGAAGGACATGCCAAATTTCCCTACCCCACTTCCCTACCC 273
QY 1836 CCAACTTTCCCAACAGCTCCACAACCCCTGTTGGAGCTACTGACGACGACGACGAC 1895
Db 274 CCAACTTTCCCAACAGCTCCACAACCCCTGTTGGAGCTACTGACGACGACGACGAC 333
QY 1896 AGTGGGTTTCCCAAGCCTTGTTCATCTCAGCCCCCAGAGATATCTGTGCTGGGAA 1955

Db 334 AGTGGGTTTCCCAAGCCTTTGTCACTCAGCCCCAGAGTATATCTGTGCTTGGGAA 393
Qy 1956 TCTCACAGAGAACTCAGAGCAACCCCTGCTGAGCTAAGGAGGTCTTATCTCTCAGG 2015
Db 394 TCTCACAGAGAACTCAGAGCAACCCCTGCTGAGCTAAGGAGGTCTTATCTCTCAGG 453
Qy 2016 GGGGTTTAAGTCCCGTTTGCAATAATGTCCTTATT 2054
Db 454 GGGGTTTAAGTCCCGTTTGCAATAATGTCCTTATT 492

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Job time : 6987.34 secs